

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
- (ii) TITLE OF INVENTION: Human Telomerase Catalytic Subunit
- (iii) NUMBER OF SEQUENCES: 727
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Townsend and Townsend and Crew LLP
 - (B) STREET: Two Embarcadero Center, Eighth Floor
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/974,549
 - (B) FILING DATE: 19-NOV-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/724,643
 - (B) FILING DATE: 01-OCT-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/844,419
 - (B) FILING DATE: 18-APR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/846,017
 - (B) FILING DATE: 25-APR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/851,843
 - (B) FILING DATE: 06-MAY-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/854,050
 - (B) FILING DATE: 09-MAY-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/911,312
 - (B) FILING DATE: 14-AUG-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/912,951
- (B) FILING DATE: 14-AUG-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/915,503
- (B) FILING DATE: 14-AUG-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: WO PCT/US97/17618
- (B) FILING DATE: 01-OCT-1997

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: WO PCT/US97/17885
- (B) FILING DATE: 01-OCT-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Apple, Randolph Ted
- (B) REGISTRATION NUMBER: 36,429
- (C) REFERENCE/DOCKET NUMBER: 015389-002610US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (415) 576-0200
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..3454
- (D) OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCG ATG      58
                                           Met
                                           1

CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC      106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
      5                      10                      15

TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC      154
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
      20                      25                      30

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CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala 35 40 45	202
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro 50 55 60 65	250
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val 70 75 80	298
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GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu 100 105 110	394
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp 115 120 125	442
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly 130 135 140 145	490
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CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu 195 200 205	682
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GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874

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GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC TGG GAC ACG CCT TGT Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys 310 315 320	1018
CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC CTC TAC TCC TCA GGC GAC Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp 325 330 335	1066
AAG GAG CAG CTG CGG CCC TCC TTC CTA CTC AGC TCT CTG AGG CCC AGC Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser 340 345 350	1114
CTG ACT GGC GCT CGG AGG CTC GTG GAG ACC ATC TTT CTG GGT TCC AGG Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg 355 360 365	1162
CCC TGG ATG CCA GGG ACT CCC CGC AGG TTG CCC CGC CTG CCC CAG CGC Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg 370 375 380 385	1210
TAC TGG CAA ATG CGG CCC CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala 390 395 400	1258
CAG TGC CCC TAC GGG GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala 405 410 415	1306
GGG GTC ACC CCA GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly 420 425 430	1354
TCT GTG GCG GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val 435 440 445	1402
CAG CTG CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val 450 455 460 465	1450
CGG GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg 470 475 480	1498
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC CTG His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu 485 490 495	1546
GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser 500 505 510	1594

GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val 515 520 525	1642
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AAG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His 595 600 605	1882
CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro 610 615 620 625	1930
AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
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GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
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Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser	Pro	
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CTG	AGG	GAT	GCC	GTC	GTC	ATC	GAG	CAG	AGC	TCC	TCC	CTG	AAT	GAG	GCC	2458
Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu	Ala	
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AGC	AGT	GGC	CTC	TTC	GAC	GTC	TTC	CTA	CGC	TTC	ATG	TGC	CAC	CAC	GCC	2506
Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	His	Ala	
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GTG	CGC	ATC	AGG	GGC	AAG	TCC	TAC	GTC	CAG	TGC	CAG	GGG	ATC	CCG	CAG	2554
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	820						825					830				
GGC	TCC	ATC	CTC	TCC	ACG	CTG	CTC	TGC	AGC	CTG	TGC	TAC	GGC	GAC	ATG	2602
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GAG	AAC	AAG	CTG	TTT	GCG	GGG	ATT	CGG	CGG	GAC	GGG	CTG	CTC	CTG	CGT	2650
Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	
850					855					860					865	
TTG	GTG	GAT	GAT	TTC	TTG	TTG	GTG	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	2698
Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	
				870					875					880		
ACC	TTC	CTC	AGG	ACC	CTG	GTC	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	2746
Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	
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Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro	
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TGG	TGC	GGC	CTG	CTG	CTG	GAT	ACC	CGG	ACC	CTG	GAG	GTG	CAG	AGC	GAC	2890
Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp	
930					935					940					945	
TAC	TCC	AGC	TAT	GCC	CGG	ACC	TCC	ATG	AGA	GCC	AGT	CTC	ACC	TTC	AAC	2938
Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr	Phe	Asn	
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Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val	
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CGAGGCTGCT ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCCAG	3651
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TCCACCCAG GGCAGCTTT TCCTCACCAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT	3771
AGTCCATCCC CAGATTCGCC ATTGTTACCC CCTCGCCCTG CCCTCCTTTG CCTTCCACCC	3831
CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC	3891
AAAGGTGTGC CCTGTACACA GGCAGGACC CTGCACCTGG ATGGGGGTCC CTGTGGGTCA	3951
AATTGGGGGG AGGTGCTGTG GGAGTAAAAT ACTGAATATA TGAGTTTTTC AGTTTTGAAA	4011
AAAA	4015

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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          35           40           45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
          50           55           60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65           70           75           80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
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Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
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Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
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Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
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Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
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Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
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Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
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Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
          210          215          220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
          225          230          235          240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
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Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
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Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

(2) INFORMATION FOR SEQ ID NO:3:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2176
- (D) OTHER INFORMATION: /note= "clone 712562"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 23..802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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TTATGTCACG GAGACCACGT TTCAAAAGAA CAGGCTCTTT TTCTACCGGA AGAGTGTCTG	120
GAGCAAGTTG CAAAGCATTG GAATCAGACA GCACTTGAAG AGGGTGCAGC TCGGGGAGCT	180
GTCGGAAGCA GAGGTCAGGC AGCATCGGGA AGCCAGGCCC GCCCTGCTGA CGTCCAGACT	240
CCGCTTCATC CCCAAGCCTG ACGGGCTGCG GCCGATTGTG AACATGGACT ACGTCGTGGG	300
AGCCAGAACG TTCCGCAGAG AAAAGAGGGC CGAGCGTCTC ACCTCGAGGG TGAAGGCACT	360
GTTCAGCGTG CTCAACTACG AGCGGGCGCG GCGCCCCGGC CTCCTGGGCG CCTCTGTGCT	420
GGGCCTGGAC GATATCCACA GGGCCTGGCG CACCTTCGTG CTGCGTGTGC GGGCCCAGGA	480
CGCGCGCCT GAGCTGTACT TTGTCAAGGT GGATGTGACG GGCGCGTACG ACACCATCCC	540
CCAGGACAGG CTCACGGAGG TCATCGCCAG CATCATCAAA CCCCAGAACA CGTACTGCGT	600
GCGTCGGTAT GCGGTGGTCC AGAAGGCCGC CCATGGGCAC GTCCGCAAGG CCTTCAAGAG	660
CCACGTCCTA CGTCCAGTGC CAGGGGATCC CGCAGGGCTC CATCCTCTCC ACGCTGCTCT	720
GGAGCCTGTG CTACGGCGAC ATGGAGAACA AGCTGTTTGC GGGGATTCCG CGGGACGGGC	780
TGCTCCTGCG TTTGGTGGAT GATTCTTGT TGGTGACACC TCACCTCACC CACGCGAAAA	840
CTTCTCTCAG GACCTGGTCC CGAGGTGTCC CTGAGTATGG CTGCGTGGTG AACTTGCGGA	900
AGACAGTGGT GAACTTCCCT GTAGAAGACG AGGCCCTGGG TGGCACGGCT TTTGTTCAGA	960
TGCGGGCCCA CGGCCTATTC CCCTGGTGCG GCCTGCTGCT GGATACCCGG ACCCTGGAGG	1020
TGCAGAGCGA CTACTCCAGC TATGCCCCGA CCTCCATCAG AGCCAGTCTC ACCTTCAACC	1080
GCGGCTTCAA GGCTGGGAGG AACATGCGTC GCAAACTCTT TGGGGTCTTG CGGCTGAAGT	1140
GTCACAGCCT GTTTCTGGAT TTGCAGGTGA ACAGCCTCCA GACGGTGTGC ACCAACATCT	1200
ACAAGATCCT CCTGCTGCAG GCGTACAGGT TTCACGCATG TGTGCTGCAG CTCCCATTTC	1260
ATCAGCAAGT TTGGAAGAAC CCCACATTTT TCCTGCGCGT CATCTCTGAC ACGGCCTCCC	1320
TCTGCTACTC CATCCTGAAA GCCAAGAACG CAGGGATGTC GCTGGGGGCC AAGGGCGCCG	1380
CCGGCCNTCT GGCCTCCGAG GCCGTGCAGT GGCTGTGCCA CCAAGCATTC CTGCTCAAGC	1440
TGACTCGACA CCGTGTCAAC TACGTGCCAC TCCTGSGGTC ACTCAGGACA GCCCAGACGC	1500
AGCTGAGTCG GAAGCTCCCG GGGACGACGC TGACTGCCCT GCAGGCCGCA GCCAACCCGG	1560
CACTGCCCTC AGACTTCAAG ACCATCCTGG ACTGATGGCC ACCCGCCCAC AGCCAGGCCG	1620


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AGAGCAGACA CCAGCAGCCC TGTCACGCCG GGCTCTACGT CCCAGGGAGG GAGGGGCGGC      1680
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GCATGTCCGG CTGAAGGCTG AGTGTCCGGC TGAGGCCTGA GCGAGTGTCC AGCCAAGGGC      1800
TGAGTGTCCA GCACACCTGC CGTCTTCACT TCCCCACAGG CTGGCGCTCG GCTCCACCCC      1860
AGGGCCAGCT TTTCCTCACC AGGAGCCCGG CTTCCTACTC CCACATAGGA ATAGTCCATC      1920
CCCAGATTCT CCATTGTTCA CCCCTCGCCC TGCCCTCCTT TGCCTTCCAC CCCCAACATC      1980
CAGGTGGAGA CCCTGAGAAG GACCCTGGGA GCTCTGGGAA TTTGGAGTGA CCAAAGGTGT      2040
GCCCTGTACA CAGGCGAGGA CCCTGCACCT GGATGGGGGT CCCTGTGGGT CAAATTGGGG      2100
GGAGGTGCTG TGGGAGTAAA ATACTGAATA TATGAGTTTT TCAGTTTTGN AAAAAAAAAA      2160
AAAAAAAAAA AAAAAA                                     2176

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3855
- (D) OTHER INFORMATION: /note= "nucleic acid sequence with an open reading frame encoding a delta-182 variant polypeptide"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..2479
- (D) OTHER INFORMATION: /product= "delta-182 variant polypeptide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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                                         Met
                                         1
CGG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC      106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His
      5                      10                      15
TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC      154
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro
      20                      25                      30

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CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala 35 40 45	202
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro 50 55 60 65	250
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val 70 75 80	298
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu 85 90 95	346
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu 100 105 110	394
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp 115 120 125	442
GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly 130 135 140 145	490
GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu 150 155 160	538
GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln 165 170 175	586
CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro 180 185 190	634
CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu 195 200 205	682
GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly 210 215 220 225	730
GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly 230 235 240	778
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala 245 250 255	826
CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT GTG GTG His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val 260 265 270	874

TCA	CCT	GCC	AGA	CCC	GCC	GAA	GAA	GCC	ACC	TCT	TTG	GAG	GGT	GCG	CTC	922
Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	Leu	
	275					280					285					
TCT	GGC	ACG	CGC	CAC	TCC	CAC	CCA	TCC	GTG	GGC	CGC	CAG	CAC	CAC	GCG	970
Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	Ala	
290					295					300					305	
GGC	CCC	CCA	TCC	ACA	TCG	CGG	CCA	CCA	CGT	CCC	TGG	GAC	ACG	CCT	TGT	1018
Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	Cys	
				310					315					320		
CCC	CCG	GTG	TAC	GCC	GAG	ACC	AAG	CAC	TTC	CTC	TAC	TCC	TCA	GGC	GAC	1066
Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	Asp	
			325					330					335			
AAG	GAG	CAG	CTG	CGG	CCC	TCC	TTC	CTA	CTC	AGC	TCT	CTG	AGG	CCC	AGC	1114
Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	Ser	
		340					345					350				
CTG	ACT	GGC	GCT	CGG	AGG	CTC	GTG	GAG	ACC	ATC	TTT	CTG	GGT	TCC	AGG	1162
Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	
	355					360					365					
CCC	TGG	ATG	CCA	GGG	ACT	CCC	CGC	AGG	TTG	CCC	CGC	CTG	CCC	CAG	CGC	1210
Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	
370					375					380					385	
TAC	TGG	CAA	ATG	CGG	CCC	CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	1258
Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	
				390					395					400		
CAG	TGC	CCC	TAC	GGG	GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	1306
Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	
			405					410					415			
GCG	GTC	ACC	CCA	GCA	GCC	GGT	GTC	TGT	GCC	CGG	GAG	AAG	CCC	CAG	GGC	1354
Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	
		420					425					430				
TCT	GTG	GCG	GCC	CCC	GAG	GAG	GAG	GAC	ACA	GAC	CCC	CGT	CGC	CTG	GTG	1402
Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	
	435					440					445					
CAG	CTG	CTC	CGC	CAG	CAC	AGC	AGC	CCC	TGG	CAG	GTG	TAC	GGC	TTC	GTG	1450
Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	
450					455					460					465	
CGG	GCC	TGC	CTG	CGC	CGG	CTG	GTG	CCC	CCA	GGC	CTC	TGG	GGC	TCC	AGG	1498
Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	
				470				475						480		
CAC	AAC	GAA	CGC	CGC	TTC	CTC	AGG	AAC	ACC	AAG	AAG	TTC	ATC	TCC	CTG	1546
His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	
			485					490					495			
GGG	AAG	CAT	GCC	AAG	CTC	TCG	CTG	CAG	GAG	CTG	ACG	TGG	AAG	ATG	AGC	1594
Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	
		500					505					510				

GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT	GGC	TGT	GTT	1642
Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
515						520					525					
CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG	GCC	AAG	TTC	CTG	1690
Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
530					535					540					545	
CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	AGG	TCT	TTC	TTT	1738
His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
				550					555					560		
TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	CTC	TTT	TTC	TAC	CGG	1786
Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	
			565					570					575			
AAG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	GGA	ATC	AGA	CAG	CAC	TTG	1834
Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	
		580					585					590				
ARG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	GAA	GCA	GAG	GTC	AGG	CAG	CAT	1882
Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	
		595				600					605					
CGG	GAA	GCC	AGG	CCC	GCC	CTG	CTG	ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	1930
Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	
610					615					620					625	
AAG	CCT	GAC	GGG	CTG	CGG	CCG	ATT	GTG	AAC	ATG	GAC	TAC	GTC	GTG	GGA	1978
Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	
			630					635						640		
GDC	AGA	ACG	TTC	CGC	AGA	GAA	AAG	AGG	GCC	GAG	CGT	CTC	ACC	TCG	AGG	2026
Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	
			645					650					655			
GTG	AAG	GCA	CTG	TTC	AGC	GTG	CTC	AAC	TAC	GAG	CGG	GCG	CGG	CGC	CCC	2074
Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	
		660					665					670				
GGC	CTC	CTG	GGC	GCC	TCT	GTG	CTG	GGC	CTG	GAC	GAT	ATC	CAC	AGG	GCC	2122
Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	
		675				680					685					
TGG	CGC	ACC	TTC	GTG	CTG	CGT	GTG	CGG	GCC	CAG	GAC	CCG	CCG	CCT	GAG	2170
Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	
690					695				700						705	
CTG	TAC	TTT	GTC	AAG	GTG	GAT	GTG	ACG	GGC	GCG	TAC	GAC	ACC	ATC	CCC	2218
Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	Pro	
				710					715					720		
CAG	GAC	AGG	CTC	ACG	GAG	GTC	ATC	GCC	AGC	ATC	ATC	AAA	CCC	CAG	AAC	2266
Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	Asn	
			725					730					735			
ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC	CAG	AAG	GCC	GCC	CAT	GGG	2314
Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	Gly	
		740					745					750				

CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA GTG CCA GGG His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly 755 760 765	2362
GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG CAG CCT GTG CTA Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu 770 775 780 785	2410
CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT TCG GCG GGA CGG GCT Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala 790 795 800	2458
GCT CCT GCG TTT GGT GGA TGATTTCTTG TTGGTGACAC CTCACCTCAC Ala Pro Ala Phe Gly Gly 805	2506
CCACGCGAAA ACCTTCCTCA GGACCCTGGT CCGAGGTGTC CCTGAGTATG GCTGCGTGGT	2566
GAACCTTGCGG AAGACAGTGG TGAACCTCCC TGTAAGAAGAC GAGGCCCTGG GTGGCACGGC	2626
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GACCCTGGAG GTGCAGAGCG ACTACTCCAG CTATGCCCGG ACCTCCATCA GAGCCAGTCT	2746
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GGGGCTGAAG TGTCACAGCC TGTTTCTGGA TTTGCAGGTG AACAGCCTCC AGACGGTGTG	2866
CACCAACATC TACAAGATCC TCCTGCTGCA GCGGTACAGG TTTCACGCAT GTGTGCTGCA	2926
GCTCCCATTT CATCAGCAAG TTTGGAAGAA CCCACATTT TTCCTGCGCG TCATCTCTGA	2986
CACGGCCTCC CTCTGCTACT CCATCCTGAA AGCCAAGAAC GCAGGGATGT CGCTGGGGGC	3046
CAAGGGGGCC GCGGGCCCTC TGCCCTCCGA GGCGGTGCGAG TGGCTGTGCC ACCAAGCATT	3106
CCTGCTCAAG CTGACTCGAC ACCGTGTAC CTACGTGCCA CTCCTGGGGT CACTCAGGAC	3166
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CAGCCAAGGG CTGAGTGTC AGCACACCTG CCGTCTTCAC TTCCCCACAG GCTGGCGCTC	3526
GGCTCCACCC CAGGGCCAGC TTTTCCTCAC CAGGAGCCCG GCTTCCACTC CCCACATAGG	3586
AATAGTCCAT CCCAGATTG GCCATTGTTT ACCCCTCGCC CTGCCCTCCT TTGCCTTCCA	3646
CCCCACCAT CCAGGTGGAG ACCCTGAGAA GGACCCTGGG AGCTCTGGGA ATTTGGAGTG	3706
ACCAAAGGTG TGCCCTGTAC ACAGGCGAGG ACCCTGCACC TGGATGGGGG TCCCTGTGGG	3766
TCAAATTGGG GGGAGGTGCT GTGGGAGTAA AATACTGAAT ATATGAGTTT TTCAGTTTTG	3826
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3855

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
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His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20           25           30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35           40           45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50           55           60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65           70           75           80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85           90           95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100           105           110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115           120           125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130           135           140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145           150           155           160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165           170           175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180           185           190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195           200           205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210           215           220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225           230           235           240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245           250           255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260           265           270

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Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala
		275					280					285			
Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His
	290					295					300				
Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro
305					310					315					320
Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly
				325					330					335	
Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro
			340					345					350		
Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser
		355					360					365			
Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln
	370					375					380				
Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His
385					390					395					400
Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg
				405					410					415	
Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln
			420					425					430		
Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu
		435					440					445			
Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe
	450					455					460				
Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser
465					470					475					480
Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser
				485					490					495	
Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met
			500					505					510		
Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys
		515					520					525			
Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe
	530					535					540				
Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe
545					550					555					560
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr
				565					570					575	
Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His
			580					585					590		

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro
 755 760 765
 Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val
 770 775 780
 Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg
 785 790 795 800
 Ala Ala Pro Ala Phe Gly Gly
 805

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..4335
- (D) OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"

(ix) FEATURE:

(A) NAME/KEY: intron
 (B) LOCATION: 2715..2818
 (D) OTHER INFORMATION: /note= "intron 1"

(ix) FEATURE:

(A) NAME/KEY: intron
 (B) LOCATION: 4173..4326
 (D) OTHER INFORMATION: /note= "intron 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCATGGGACC CACTGCAGGG GCAGCTGGGA GGCTGCAGGC TTCAGGTCCC AGTGGGGTTG	60
CCATCTGCCA GTAGAAACCT GATGTAGAAT CAGGGCGCGA GTGTGGACAC TGCCTGAAT	120
CTCAATGTCT CAGTGTGTGC TGAAACATGT AGAAATTAAA GTCCATCCCT CCTACTCTAC	180
TGGGATTGAG CCCCTTCCCT ATCCCCCCCC AGGGGCAGAG GAGTTCCTCT CACTCCTGTG	240
GAGGAAGGAA TGATACTTTG TTATTTTTCA CTGCTGGTAC TGAATCCACT GTTTCATTTG	300
TTGGTTTGTT TGTTTTGTTT TGAGAGGCGG TTCACTCTT GTTGCTCAGG CTGGAGGGAG	360
TGCAATGGCG CGATCTTGGC TTA CTGCAGC CTCTGCCTCC CAGGTTCAAG TGATTCTCCT	420
GCTTCGCGCT CCCATTGGC TGGGATTACA GGCACCGCC ACCATGCCCA GCTAATTTTT	480
TGTATTTTGA GTAGAGACGG GGGTGGGGGT GGGGTTCAAC ATGTTGGCCA GGCTGGTCTC	540
GAACTTCTGA CCTCAGATGA TCCACCTGCC TCTGCCTCCT AAAGTGCTGG GATTACAGGT	600
GTGAGCCACC ATGCCAGCT CAGAATTTAC TCTGTTTAGA AACATCTGGG TCTGAGGTAG	660
GAGGCTCACC CCACTCAAGT GTTGTGGTGT TTTAAGCCAA TGATAGAATT TTTTATTGT	720
TGTTAGAACA CTCTTGATGT TTTACACTGT GATGACTAAG ACATCATCAG CTTTTCAAAG	780
ACACACTAAC TGCACCCATA ATACTGGGGT GTCTTCTGGG TATCAGCGAT CTTCATTGAA	840
TGCCGGGAGG CGTTTCCTCG CCATGCACAT GGTGTTAATT ACTCCAGCAT AATCTTCTGC	900
TTCCATTTCT TCTCTCCCT CTTTTAAAT TGTGTTTCT ATGTTGGCTT CTCTGCAGAG	960
AACCAGTGTA AGCTACAAC TAACTTTTGT TGGAAACAAAT TTTCCAAACC GCCCCTTTC	1020
CCTAGTGGCA GAGACAATTC ACAAACACAG CCCTTTAAAA AGGCTTAGGG ATCACTAAGG	1080
GGATTTCTAG AAGAGCGACC CGTAATCCTT AAGTATTTAC AAGACGAGGC TAACCTCCAG	1140
CGAGCGTGAC AGCCAGGGA GGGTGCGAGG CCTGTTCAAA TGCTAAGCTT CCATAAATAA	1200
AGCAAATTTT CTCCGGCAGT TTCTGGAAAG TAGGAAAGGT TAACATTTAA GGTGCGTTT	1260
GTTAGCATTT CAGTGTGTC CGACCTCAGC TAACAGCATC CCTGCAAGGC CTCGGGAGAC	1320
CCAGAAGTTT CTCGCCCTT AGATCCAAAC TTGAGCAACC CGGAGTCTGG ATCCTGGGA	1380
AGTCTCAGC TGCCTGCGG TTGTGCCGGG GCCCCAGGTC TGGAGGGGAC CAGTGGCCGT	1440

GTGGCTTCTA CTGCTGGGCT GGAAGTCGGG CCTCCTAGCT CTGCAGTCCG AGGCTTGGAG	1500
CCAGGTGCCT GGACCCCGAG GCTGCCCTCC ACCCTGTGCG GCGGGGATGT GACCAGATGT	1560
TGGCCTCATC TGCCAGACAG AGTGCCGGGG CCCAGGGTCA AGGCCGTTGT GGCTGGTGTG	1620
AGGCGCCCGG TGC GCGGCCA GCAGGAGCGC CTGGCTCCAT TTCCCACCCT TTCTCGACGG	1680
GACCGCCCCG GTGGGTGATT AACAGATATT GGGGTGGTTT GCTCATGGTG GGGACCCCTT	1740
CGCCGCCTGA GAACCTGCAA AGAGAAATGA CGGGCCTGTG TCAAGGAGCC CAAGTCGCGG	1800
GGAAGTGTTG CAGGGAGGCA CTCCGGGAGG TCCCGCGTGC CCGTCCAGGG AGCAATGCGT	1860
CCTCGGGTTC GTCCCCAGCC GCGTCTACGC GCCTCCGTCC TCCCCTTCAC GTCCGGCATT	1920
CGTGGTGCCC GGAGCCCGAC GCGCCGCGTC CGGACCTGGA GGCAGCCCTG GGTCTCCGGA	1980
TCAGGCCAGC GGCCAAAGGG TCGCCGCACG CACCTGTTC CAGGGCCTCC ACATCATGGC	2040
CCCTCCCTCG GGTACCCCA CAGCCTAGGC CGATTGACC TCTCTCCGCT GGGGCCCTCG	2100
CTGGCGTCCC TGCACCCTGG GAGCGCGAGC GCGCGCGGG CGGGGAAGCG CGGCCAGAC	2160
CCCCGGGTCC GCGCGGAGCA GCTGCGCTGT CGGGGCCAGG CCGGGCTCCC AGTGGATTCT	2220
CGGGCAACAG ACGCCAGGA CCGCGCTTC CACGTGGCGG AGGACTGGG GACCCGGGCA	2280
CCGSTCCTGC CCCTTCACCT TCCAGCTCCG CCTCGTCCG GCGGAACCCG GCGCGTCCC	2340
GAACCTTCC CGGGTCCCCG GCGCAGCCCC TTCCGGGCCA TCCAGCCCG TCCCGTTCCT	2400
TTTCCGCGGC CCGGCCCTCT CCTCGCGGGC CGAGTTTCAG GCAGCGCTGC GTCTGTCTGC	2460
GCAAGTGGGA AGCCCTGGCC CCGGCCACCC CCGCGATGCC GCGCGTCCC CGCTGCCGAG	2520
CCGTGCGCTC CCTGTGCGC AGCCACTACC GCGAGGTGCT GCGCTGGCC ACGTTCGTGC	2580
GGCGCTGGG GCGCCAGGGC TGGCGGCTGG TGCAGCGCGG GAGCCCGGG GCTTTCGCGG	2640
CGTGGTGGC CAGTGCCTG GTGTGCGTGC CCTGGGACGC ACGGCCGCC CCCGCCGCC	2700
CCTCCTTCCG CCAGGTGGGC CTCCCCGGGG TCGCGTCCG GCTGGGGTTG AGGGCGGCCG	2760
GGGGGAACCA GCGACATGC GAGAGCAGC CAGGCGACTC AGGGCGCTT CCGCGCAGGT	2820
GTCTGCCTG AAGGAGCTGG TGGCCCGAGT GCTGCAGAGG CTGTGCGAGC GCGGCGCGAA	2880
GAACGTGCTG GCCTTCGGCT TCGCGTGTG GGACGGGGCC CGCGGGGGCC CCGCGAGGC	2940
CTTCACCACC AGCGTGCGCA GCTACCTGCC CAACACGGTG ACCGACGCAC TGCGGGGGAG	3000
CGGGCGGTGG GGGCTGCTGC TCGCCGCGT GGGCGACGAC GTGCTGGTTC ACCTGCTGSC	3060
ACGTGCGCG CTCTTTGTG TGGTGGCTCC CAGCTGCGCC TACCAGGTGT GCGGGCCGSC	3120
GCTGTACCAG CTCGGCGCTG CCACTCAGGC CCGCCCCCG CCACACGCTA GTGGACCCCG	3180
AAGGCGTCTG GGATGCGAAC GGGCCTGGAA CCATAGCGTC AGGGAGGCCG GGGTCCCCCT	3240
GGGCCTGCCA GCGCGGGTG CGAGGAGGCG CGGGGGCAGT GCCAGCCGAA GTCTGCCGTT	3300

GCCCAAGAGG CCCAGGCGTG GCGCTGCCCC TGAGCCGGAG CGGACGCCCC TTGGGCAGGG	3360
GTCCTGGGCC CACCCGGGCA GGACGCGTGG ACCGAGTGAC CGTGGTTTCT GTGTGGTGTC	3420
ACCTGCCAGA CCCGCCGAAG AAGCCACCTC TTTGGAGGGT GCGCTCTCTG GCACGCGCCA	3480
CTCCCACCCA TCCGTGGGCC GCCAGCACCA CGCGGGCCCC CCATCCACAT CGCGGCCACC	3540
ACGTCCCTGG GACACGCCTT GTCCCCCGGT GTACGCCGAG ACCAAGCACT TCCTCTACTC	3600
CTCAGGCGAC AAGGAGCAGC TGCGGCCCTC CTTCTACTC AGCTCTCTGA GGCCCAGCCT	3660
GACTGGCGCT CGGAGGCTCG TGGAGACCAT CTTTCTGGGT TCCAGGCCCT GGATGCCAGG	3720
GACTCCCCGC AGGTTGCCCC GCCTGCCCCA GCGCTACTGG CAAATGCGGC CCCTGTTTCT	3780
GGAGCTGCTT GGAACACAG CGCAGTGCCC CTACGGGGTG CTCCTCAAGA CGCACTGCCC	3840
GCTGCGAGCT GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC	3900
TGTGGCGGCC CCCGAGGAGG AGGACACAGA CCCCCGTCGC CTGGTGCAGC TGCTCCGCCA	3960
GCACAGCAGC CCCTGGCAGG TGTACGGCTT CGTGCGGGCC TGCCTGCGCC GGCTGGTGCC	4020
CCCAGGCCTC TGGGGCTCCA GGCACAACGA ACGCCGCTTC CTCAGGAACA CCAAGAAGTT	4080
CATCTCCCTG GGAAGCATG CCAAGCTCTC GCTGCAGGAG CTGACGTGGA AGATGAGCGT	4140
GCGGGACTGC GCTTGCTGC GCAGGAGCCC AGGTGAGGAG GTGGTGGCCG TCGAGGGCCC	4200
AGGCCCCAGA GCTGAATGCA GTAGGGGCTC AGAAAAGGGG GCAGGCAGAG CCCTGGTCCT	4260
CCTGTCTCCA TCGTCACGTG GGCACACGTG GCTTTTCGCT CAGGACGTCG AGTGGACACG	4320
GTGATCGAGG TCGAC	4335

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 95..198
- (D) OTHER INFORMATION: /note= "intron 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGACCCGGCG GCTTCCGCG CGCTGGTGGC CCAAGTCCTG GTGTGCGTGC CCTGGGACGC	60
ACGGCCGCCC CCCGCCGCC CCTCCTTCG CCAGGTGGGC CTCCCGGGG TCGGCGTCCG	120
GCTGGGGTTG AGGGCGGCCG GGGGAACCA GCGACATGCG GAGAGCAGCG CAGGCGACTC	180

AGGGCGCTTC CCCCGCAGGT GTCCTGCCTG AAGGAGCTGG TGGCCCGAGT GCTGCAGAGG 240

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: /note= "expressed sequence tag (EST)
AA281296"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCAAGTTCC TGCCTGGCT GATGAGTGTG TACGTCGTCG AGCTGCTCAG GTCTTTCTTT	60
TATGTCACGG AGACCACGTT TCAAAAGAAC AGGCTCTTTT TCTACCGGAA GAGTGTCTGG	120
AGCAAGTTGC AAAGCATTGG AATCAGACAG CACTTGAAGA GGGTGCAGCT GCGGGACGTG	180
TCGGAAGCAG AGGTCAGGCA GCATCGGGAA GCCAGGCCCG CCCTGCTGAC GTCCAGACTC	240
CGCTTCATCC CCAAGCCTGA CGGGCTGCGG CCGATTGTGA ACATGGACTA CGTCGTGGGA	300
GCCAGAACGT TCCGCAGAGA AAAGAGGGCC GAGCGTCTCA CCTCGAGGGT GAAGGCACTG	360
TTGAGCGTGC TCAACTACGA GCGGGCGCG	389

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: /note= "182 basepair sequence deleted in
clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCTAOCCTGA CAGACCTCCA GCCGTACATG CGACAGTTCG TGGCTCACCT GCAGGAGACC	60
AGCCCCGTGA GGGATGCCGT CGTCATCGAG CAGAGCTCCT CCCTGAATGA GGCCAGCAGT	120

GGCCTCTTCG ACGTCTTCCT ACGCTTCATG TGCCACCACG CCGTGCGCAT CAGGGGCAAG 180

TC 182

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..259
- (D) OTHER INFORMATION: /note= "protein encoded by clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr
1 5 10 15

Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val
20 25 30

Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val
35 40 45

Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala
50 55 60

Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp
65 70 75 80

Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr
85 90 95

Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala
100 105 110

Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu
115 120 125

Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr
130 135 140

Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe
145 150 155 160

Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg
165 170 175

Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys
180 185 190

Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg
 195 200 205

Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro Ala
 210 215 220

Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg His
 225 230 235 240

Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro Ala
 245 250 255

Phe Gly Gly

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Trp
1           5           10           15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
          20           25           30

Xaa Trp

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Trp
1          5          10          15
Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
20          25          30
Xaa Xaa Trp
35

```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: /note= "TRT motifs from human"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
1          5          10          15
Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
20          25          30
Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
35          40          45
Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
50          55          60
Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
65          70          75          80
Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
85          90          95

```


Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 100 105 110

Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 115 120 125

Ala

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from
 Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys
 1 5 10 15

Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe
 20 25 30

Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe
 35 40 45

Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe
 50 55 60

Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met
 65 70 75 80

Lys Met Glu Ala Phe Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp
 85 90 95

Thr Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys
 100 105 110

Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile
 115 120 125

Lys Met Gly Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu
 130 135 140

Arg Pro Val Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser
 145 150 155 160

Gly Ile Pro Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys
 165 170 175

Lys Asp Leu Leu Lys His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val
 180 185 190

Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met
 195 200 205

Phe Arg Ile Val Lys Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg
 210 215 220

Lys Tyr Ala Thr Ile His Ala Thr Ser
 225 230

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from *Saccharomyces cerevisiae* EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys
 1 5 10 15

His Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp
 20 25 30

Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys
 35 40 45

Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr
 50 55 60

Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr
 65 70 75 80

Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser
 85 90 95

Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn
 100 105 110

Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu
 115 120 125

Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln
 130 135 140

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Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val Asn Ser Asp
 115 120 125
 Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu Asn Ser His
 130 135 140
 Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp Pro Phe Gly
 145 150 155 160
 Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr Glu Glu Phe
 165 170 175
 Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe Phe Ala Thr
 180 185 190
 Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg Glu Lys Leu Ser
 195 200 205
 Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp Phe Trp Ile Met
 210 215 220
 Thr Ala Gln Ile Leu Lys Arg Lys Asn
 225 230

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif T"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly, Ser, Thr, Tyr, Cys, Asn or Gln"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Xaa Phe Phe Tyr
 1

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..7
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Xaa Arg Xaa Ile Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif 2"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 3

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Phe Arg Xaa Ile

1

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..6

(D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
from motif A"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = charged amino acid, Asp,
Glu, His, Lys or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 6

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Pro Xaa Leu Tyr Phe Xaa

1

5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..6

(D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
from motif B'"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Ile Pro Gln Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..4

(D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
from motif C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Leu Arg Leu
1

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..7

(D) OTHER INFORMATION: /note= "consensus telomerase RT sequence
from motif C"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Asp	Asp	Phe	Leu	Xaa	Ile	Thr
1				5		

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..48

(D) OTHER INFORMATION: /note= "motif T peptide from
Schizosaccharomyces pombe TRT tezl p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp	Leu	Tyr	Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr
1				5				10						15	

Ile	Thr	Glu	Ser	Ser	Asp	Leu	Arg	Asn	Arg	Thr	Val	Tyr	Phe	Arg	Lys
		20						25						30	

Asp	Ile	Trp	Lys	Leu	Leu	Cys	Arg	Pro	Phe	Ile	Thr	Ser	Met	Lys	Met
		35						40					45		

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..54

(D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
Schizosaccharomyces pombe TRT tezl p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr Leu Pro Pro Ala Val
 1 5 10 15
 Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu
 20 25 30
 Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn Lys Lys Met Leu Val
 35 40 45
 Ser Thr Asn Gln Thr Leu
 50

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from
 Schizosaccharomyces pombe TRT te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr
 1 5 10 15
 Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys Lys Leu
 20 25 30
 Lys Asp

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from
 Schizosaccharomyces pombe TRT te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser
 1 5 10 15
 Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu
 20 25 30
 Ser Phe Thr
 35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "motif C and D peptide from
 Schizosaccharomyces pombe TRT te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys
 1 5 10 15
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His
 20 25 30
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile
 35 40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from
 Schizosaccharomyces pombe TRT te2lp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "motif T peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr
 1 5 10 15
 Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys
 20 25 30
 Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
 1 5 10 15
 Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
 20 25 30

Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
 35 40 45

Arg Leu Thr Ser Arg Val
 50

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 1 5 10 15

Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 20 25 30

Lys Pro

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser
 1 5 10 15

Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe
 20 25 30

Ala Gly Ile
35

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "motif C and D peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr
1				5						10					15
His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr
			20					25					30		
Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val					
		35					40								

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "motif T peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1           5           10           15
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
          20           25           30
Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys
          35           40           45

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys
1           5           10           15
Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe
          20           25           30
Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr
          35           40           45
Asn Thr Lys Leu Leu Asn
          50

```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr
1           5           10           15
Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys
20           25           30
Leu Leu

```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser
1           5           10           15
Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu
20           25           30
Gly Phe Leu
35

```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "motif C and D peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn
1           5           10           15
Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu Asn
          20           25           30
Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr
          35           40

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser Ile
1           5           10

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: /note= "motif T peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Trp	Leu	Phe	Arg	Gln	Leu	Ile	Pro	Lys	Ile	Ile	Gln	Thr	Phe	Phe	Tyr
1					5				10					15	
Cys	Thr	Glu	Ile	Ser	Ser	Thr	Val	Thr	Ile	Val	Tyr	Phe	Arg	His	Asp
			20					25					30		
Thr	Trp	Asn	Lys	Leu	Ile	Thr	Pro	Phe	Ile	Val	Glu	Tyr	Phe	Lys	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /note= "motif 1 peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Cys	Arg	Asn	His	Asn	Ser	Tyr	Thr	Leu	Ser	Asn	Phe	Asn	His	Ser	Lys
1				5					10					15	
Met	Arg	Ile	Ile	Pro	Lys	Lys	Ser	Asn	Asn						
			20					25							

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..29

(D) OTHER INFORMATION: /note= "motif 2 peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe	Arg	Ile	Ile	Ala	Ile	Pro	Cys	Arg	Gly	Ala	Asp	Glu	Glu	Glu	Phe
1				5					10					15	

Thr	Ile	Tyr	Lys	Glu	Asn	His	Lys	Asn	Ala	Ile	Gln	Pro
			20					25				

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..34

(D) OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Val	Leu	Pro	Glu	Leu	Tyr	Phe	Met	Lys	Phe	Asp	Val	Lys	Ser	Cys	Tyr
1				5					10					15	

Asp	Ser	Ile	Pro	Arg	Met	Glu	Cys	Met	Arg	Ile	Leu	Lys	Asp	Ala	Leu
			20					25					30		

Lys Asn

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: /note= "motif B' peptide from
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Lys Glu Leu Glu Val Trp Lys His Ser Ser Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "consensus non-telomerase RT -
sequence from motif B'"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Xaa Pro Gln Gly
 1

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "consensus non-telomerase RT
sequence from motif C"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp Asp Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Leu Ser Asn Glu Leu Gly Thr Gly Lys Phe Lys Phe Lys Pro Met Arg
1 5 10 15

Ile Val Asn Ile Pro Lys Pro Lys Gly Gly Ile Arg Pro Leu Ser Val
20 25 30

Gly Asn Pro Arg Asp Lys Ile Val Gln Glu Val Met Arg Met Ile Leu
35 40 45

Asp Thr Ile Phe Asp Lys Lys
50 55

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Phe Gly Gly Ser Asn Trp Phe Ile Glu Val Asp Leu Lys Lys Cys Phe
1 5 10 15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile
20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B' peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Thr Tyr His Lys Pro Met Leu Gly Leu Pro Gln Gly Ser Leu Ile Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:54:

(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..17

(D) OTHER INFORMATION: /note= "motif C peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Tyr Val Arg Tyr Ala Asp Asp Ile Leu Ile Gly Val Leu Gly Ser Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

(A) LENGTH: 25 amino acids
(B) TYPE: amino acid-
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..25

(D). OTHER INFORMATION: /note= "motif D peptide from
Saccharomyces cerevisiae cytochrome
oxidase group II intron 1-encoded
mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Lys Met Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly Leu
1 5 10 15

Thr Ile Asn Glu Glu Lys Thr Leu Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from
 Saccharomyces cerevisiae cytochrome
 oxidase group II intron 1-encoded
 mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Glu Thr Pro Ala Arg Phe Leu Gly Tyr Asn Ile
 1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 1 peptide from
 Drosophila melanogaster TART non-LTR
 retrotransposable element reverse
 transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ser Ile Leu Arg Ile Gly Tyr Tyr Pro Asp Ala Trp Lys His Ala Gln
 1 5 10 15

Val Lys Met Ile Leu Lys Pro Gly Lys Ser
 20 25

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "motif 2 peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Tyr Arg Pro Ile Ser Leu Leu Ser Gly Leu Ser Lys Met Phe Glu Arg
 1 5 10 15
 Leu Leu Leu Lys Arg Leu Phe Arg Val Asp Leu Phe Lys
 20 25

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Arg Lys Glu Tyr Cys Ser Ala Val Phe Leu Asp Ile Ser Glu Ala Phe
 1 5 10 15
 Asp Arg Val Trp His Glu Gly Leu Leu Leu Lys Leu Ala Lys Ile Leu
 20 25 30
 Pro Tyr

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(E) LOCATION: 1..35

(D) OTHER INFORMATION: /note= "motif B' peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Arg Ala Gly Gln Ile Gly Ala Gly Val Pro Gln Gly Ser Asn Leu Gly
1 5 10 15

Pro Ile Leu Tyr Ser Ile Phe Ser Ser Asp Met Pro Leu Pro His Ile
20 25 30

Tyr His Pro
35

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(3) LOCATION: 1..17

(D) OTHER INFORMATION: /note= "motif C peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Leu Ser Thr Tyr Ala Asp Asp Thr Ile Val Leu Ser Ser Asp Ile Leu
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif D peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

Asn Glu Asn Tyr Leu Lys Thr Phe Ser Asp Trp Ala Asp Lys Trp Gly
1           5           10           15

Ile Ser Val Asn Ala Ala Lys Thr Gly His
          20           25

```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from
Drosophila melanogaster TART non-LTR
retrotransposable element reverse
transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

Glu Ser Lys Gln Ser Tyr Leu Gly Val Ile Leu
1           5           10

```

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: Peptide
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /note= "motif 1 peptide from HIV-1
 reverse transcriptase"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro  
1 5 10 15

Val Phe Ala Ile Lys Lys Lys Asp Ser Thr  
20 25

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1.63  
(D) OTHER INFORMATION: /note= "motif 2 and A peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp  
1                   5                   10                   15

Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys  
20 25 30

Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val  
35 40 45

Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro  
50 55 60

(2) INFORMATION FOR SEO ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 35  
(D) OTHER INFORMATION: /note= "motif B' peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser  
1 5 10 15

Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Lys  
20 25 30

Lys Gln Asn  
35

(2) INFORMATION FOR SEQ ID NO: 67:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..17  
(D) OTHER INFORMATION: /note= "motif C peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile  
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..37  
(D) OTHER INFORMATION: /note= "motif D and E peptide from HIV-1 reverse transcriptase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly  
1 5 10 15

Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp  
20 25 30

Met Gly Ile Thr Leu  
35

(2) INFORMATION FOR SEQ ID NO: 69:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide .

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..4  
(D) OTHER INFORMATION: /note= "consensus telomerase RT finger  
sequence from motif 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ile Pro Lys Lys  
1

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..5

(D) OTHER INFORMATION: /note= "consensus telomerase RT palm,  
primer grip sequence from motif C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Leu Leu Leu Arg Leu  
1 5

- (2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..4

(D) OTHER INFORMATION: /note= "consensus telomerase RT palm,  
primer grip sequence from motif C"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp Asp Phe Leu  
1

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: /note= "telomerase specific motif T  
peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr  
1 5 10 15

Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys  
20 25 30

Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile  
35 40

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..5  
(D) OTHER INFORMATION: /note= "telomerase specific motif T'  
peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Glu Ala Glu Val Arg  
1 5

## (2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1.16  
(D) OTHER INFORMATION: /note= "telomerase RT finger motif  
1 and 2 peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val  
1 5 10 15



## (2) INFORMATION FOR SEQ ID NO:75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif A peptide from human TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr  
 1                    5                    10                    15  
 Ile

## (2) INFORMATION FOR SEQ ID NO:76:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B' peptide from human TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu  
 1                    5                    10                    15  
 Leu Cys Ser Leu Cys Tyr  
 20

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..13

(D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif C peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..16

(D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif D peptide from human TRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..11

(D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif E peptide from human TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Trp Cys Gly Leu Leu Asp Thr Arg Thr Leu  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "telomerase specific motif T  
peptide from Schizosaccharomyces  
pombe TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr  
 1                      5                      10                      15

Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys  
                     20                      25                      30

Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile  
                     35                      40

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "telomerase specific motif T'  
peptide from Schizosaccharomyces  
pombe TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Glu Asn Asn Val Arg  
 1                      5

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif  
1 and 2 peptide from Schizosaccharomyces  
pombe TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Ile | Arg | Leu | Leu | Pro | Lys | Lys | Asn | Thr | Phe | Arg | Leu | Ile | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif A  
peptide from Schizosaccharomyces  
pombe TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Lys | Tyr | Phe | Val | Arg | Ile | Asp | Ile | Lys | Ser | Cys | Tyr | Asp | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Ile

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B'  
peptide from Schizosaccharomyces  
pombe TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe  
 1                      5                      10                      15

Leu Cys His Phe Tyr Met  
                     20

## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip  
motif C peptide from Schizosaccharomyces  
pombe TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip  
motif D peptide from Schizosaccharomyces  
pombe TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gly Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif E peptide from Schizosaccharomyces pombe TRT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "telomerase specific motif T peptide from Euplotes aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr  
 1 5 10 15

Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys  
 20 25 30

Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile  
 35 40

## (2) INFORMATION FOR SEQ ID NO:89:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "telomerase specific motif T'  
peptide from Euplotes aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Glu Lys Glu Val Glu  
1 5

## (2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif  
1 and 2 peptide from Euplotes  
aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif A peptide from Euplotes aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser  
 1                      5                      10                      15

Val

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B' peptide from Euplotes aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile  
 1                      5                      10                      15

Leu Ser Ser Phe Tyr Tyr  
 20

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif C peptide from Euplotes aediculatus p123"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..16  
(D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif D peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..11  
(D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip  
motif E peptide from Euplotes  
aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Trp Ile Gly Ile Ser Ile Asp Met Lys Thr Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "telomerase specific motif T  
peptide from Saccharomyces  
cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr  
1                      5                      10                      15

Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp  
                    20                      25                      30

Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile  
                    35                      40

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "telomerase specific motif T'  
peptide from Saccharomyces  
cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Glu Asn Asn Val Cys  
1                      5

(2) INFORMATION FOR SEQ ID NO:98:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 11 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
    (A) NAME/KEY: Peptide
    (B) LOCATION: 1..11
    (D) OTHER INFORMATION: /note= "telomerase RT finger motif 1
                           peptide from Saccharomyces
                           cerevisiae EST2"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 99:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..5
 (D) OTHER INFORMATION: /note= "telomerase RT finger motif 2
 peptide from Saccharomyces
 cerevisiae EST2"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe Arg Ile Ile Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif A peptide from Saccharomyces cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser  
 1                      5                      10                      15  
 Ile

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "telomerase RT finger motif B' peptide from Saccharomyces cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro  
 1                      5                      10                      15  
 Ile Val Asp Leu Val Tyr  
 20

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide.
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif C peptide from Saccharomyces cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip  
 motif D peptide from Saccharomyces  
 cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "telomerase RT palm, primer grip  
 motif E peptide from Saccharomyces  
 cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Trp Lys His Ser Ser Thr Met Asn Asn Phe His  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: protein\_bind
- (B) LOCATION: 1..10
- (D) OTHER INFORMATION: /note= "NFkappaB CS1 binding site motif"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGGRHTYYHC

10

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: protein\_bind
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "NFkappaB MHC I.2 binding site motif"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGGGCTTCCC C

11

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: protein\_bind
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "NFkappaB CS2 binding site motif"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

RGGGRMTYYC C

11

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: protein\_bind
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "topoisomerase II cleavage site motif"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

RNYNNCNNGY NGKTNVNY

18

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 101..3196
- (D) OTHER INFORMATION: /note= "Euplotes aediculatus 123 kDa telomerase protein subunit (TRT)"  
/codon= (seq: "tga", aa: Cys)  
/product= "Euplotes aediculatus 123 kDa telomerase protein subunit (TRT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AAACCCCCAA AACCCCAAAA CCCCTTTT TAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA 60

TTAATAAGCT CAGATTTTAA ATATTAATTA CAAACCTAA ATG GAG GTT GAT GTT 115  
Met Glu Val Asp Val  
1 5

GAT AAT CAA GCT GAT AAT CAT GGC ATT CAC TCA GCT CTT AAG ACT TGT 163  
Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala Leu Lys Thr Cys  
10 15 20

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GAA GAA ATT AAA GAA GCT AAA ACG TTG TAC TCT TGG ATC CAG AAA GTT<br>Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp Ile Gln Lys Val<br>25 30 35        | 211 |
| ATT AGA TGA AGA AAT CAA TCT CAA AGT CAT TAT AAA GAT TTA GAA GAT<br>Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys Asp Leu Glu Asp<br>40 45 50        | 259 |
| ATT AAA ATA TTT GCG CAG ACA AAT ATT GTT GCT ACT CCA CGA GAC TAT<br>Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr Pro Arg Asp Tyr<br>55 60 65        | 307 |
| AAT GAA GAA GAT TTT AAA GTT ATT GCA AGA AAA GAA GTA TTT TCA ACT<br>Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu Val Phe Ser Thr<br>70 75 80 85     | 355 |
| GGA CTA ATG ATC GAA CTT ATT GAC AAA TGC TTA GTT GAA CTT CTT TCA<br>Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val Glu Leu Leu Ser<br>90 95 100       | 403 |
| TCA AGC GAT GTT TCA GAT AGA CAA AAA CTT CAA TGA TTT GGA TTT CAA<br>Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys Phe Gly Phe Gln<br>105 110 115     | 451 |
| CTT AAG GGA AAT CAA TTA GCA AAG ACC CAT TTA TTA ACA GCT CTT TCA<br>Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu Thr Ala Leu Ser<br>120 125 130     | 499 |
| ACT CAA AAG CAG TAT TTC TTT CAA GAC GAA TGG AAC CAA GTT AGA GCA<br>Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn Gln Val Arg Ala<br>135 140 145     | 547 |
| ATG ATT GGA AAT GAG CTC TTC CGA CAT CTC TAC ACT AAA TAT TTA ATA<br>Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr Lys Tyr Leu Ile<br>150 155 160 165 | 595 |
| TTC CAG CGA ACT TCT GAA GGA ACT CTT GTT CAA TTT TGC GGG AAT AAC<br>Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe Cys Gly Asn Asn<br>170 175 180     | 643 |
| GTT TTT GAT CAT TTG AAA GTC AAC GAT AAG TTT GAC AAA AAG CAA AAA<br>Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp Lys Lys Gln Lys<br>185 190 195     | 691 |
| GGT GGA GCA GCA GAC ATG AAT GAA CCT CGA TGT TGA TCA ACC TGC AAA<br>Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys Ser Thr Cys Lys<br>200 205 210     | 739 |
| TAC AAT GTC AAG AAT GAG AAA GAT CAC TTT CTC AAC AAC ATC AAC GTG<br>Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn Asn Ile Asn Val<br>215 220 225     | 787 |
| CCG AAT TGG AAT AAT ATG AAA TCA AGA ACC AGA ATA TTT TAT TGC ACT<br>Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile Phe Tyr Cys Thr<br>230 235 240 245 | 835 |
| CAT TTT AAT AGA AAT AAC CAA TTC TTC AAA AAG CAT GAG TTT GTG AGT<br>His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His Glu Phe Val Ser<br>250 255 260     | 883 |



|                                                                 |      |
|-----------------------------------------------------------------|------|
| AAC AAA AAC AAT ATT TCA GCG ATG GAC AGA GCT CAG ACG ATA TTC ACG | 931  |
| Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln Thr Ile Phe Thr |      |
| 265 270 275                                                     |      |
| AAT ATA TTC AGA TTT AAT AGA ATT AGA AAG AAG CTA AAA GAT AAG GTT | 979  |
| Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu Lys Asp Lys Val |      |
| 280 285 290                                                     |      |
| ATC GAA AAA ATT GCC TAC ATG CTT GAG AAA GTC AAA GAT TTT AAC TTC | 1027 |
| Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys Asp Phe Asn Phe |      |
| 295 300 305                                                     |      |
| AAC TAC TAT TTA ACA AAA TCT TGT CCT CTT CCA GAA AAT TGG CGG GAA | 1075 |
| Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu Asn Trp Arg Glu |      |
| 310 315 320 325                                                 |      |
| CGG AAA CAA AAA ATC GAA AAC TTG ATA AAT AAA ACT AGA GAA GAA AAG | 1123 |
| Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr Arg Glu Glu Lys |      |
| 330 335 340                                                     |      |
| TCG AAG TAC TAT GAA GAG CTG TTT AGC TAC ACA ACT GAT AAT AAA TGC | 1171 |
| Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr Asp Asn Lys Cys |      |
| 345 350 355                                                     |      |
| GTC ACA CAA TTT ATT AAT GAA TTT TTC TAC AAT ATA CTC CCC AAA GAC | 1219 |
| Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile Leu Pro Lys Asp |      |
| 360 365 370                                                     |      |
| TTT TTG ACT GGA AGA AAC CGT AAG AAT TTT CAA AAG AAA GTT AAG AAA | 1267 |
| Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys Lys Val Lys Lys |      |
| 375 380 385                                                     |      |
| TAT GTG GAA CTA AAC AAG CAT GAA CTC ATT CAC AAA AAC TTA TTG CTT | 1315 |
| Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys Asn Leu Leu Leu |      |
| 390 395 400 405                                                 |      |
| GAG AAG ATC AAT ACA AGA GAA ATA TCA TGG ATG CAG GTT GAG ACC TCT | 1363 |
| Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser |      |
| 410 415 420                                                     |      |
| GCA AAG CAT TTT TAT TAT TTT GAT CAC GAA AAC ATC TAC GTC TTA TGG | 1411 |
| Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp |      |
| 425 430 435                                                     |      |
| AAA TTG CTC CGA TGG ATA TTC GAG GAT CTC GTC GTC TCG CTG ATT AGA | 1459 |
| Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg |      |
| 440 445 450                                                     |      |
| TGA TTT TTC TAT GTC ACC GAG CAA CAG AAA AGT TAC TCC AAA ACC TAT | 1507 |
| Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr |      |
| 455 460 465                                                     |      |
| TAC TAC AGA AAG AAT ATT TGG GAC GTC ATT ATG AAA ATG TCA ATC GCA | 1555 |
| Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala |      |
| 470 475 480 485                                                 |      |
| GAC TTA AAG AAG GAA ACG CTT GCT GAG GTC CAA GAA AAA GAG GTT GAA | 1603 |
| Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu |      |
| 490 495 500                                                     |      |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GAA TGG AAA AAG TCG CTT GGA TTT GCA CCT GGA AAA CTC AGA CTA ATA | 1651 |
| Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile |      |
| 505 510 515                                                     |      |
| CCG AAG AAA ACT ACT TTC CGT CCA ATT ATG ACT TTC AAT AAG AAG ATT | 1699 |
| Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile |      |
| 520 525 530                                                     |      |
| GTA AAT TCA GAC CGG AAG ACT ACA AAA TTA ACT ACA AAT ACG AAG TTA | 1747 |
| Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu |      |
| 535 540 545                                                     |      |
| TTG AAC TCT CAC TTA ATG CTT AAG ACA TTG AAG AAT AGA ATG TTT AAA | 1795 |
| Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys |      |
| 550 555 560 565                                                 |      |
| GAT CCT TTT GGA TTC GCT GTT TTT AAC TAT GAT GAT GTA ATG AAA AAG | 1843 |
| Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys |      |
| 570 575 580                                                     |      |
| TAT GAG GAG TTT GTT TGC AAA TGG AAG CAA GTT GGA CAA CCA AAA CTC | 1891 |
| Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu |      |
| 585 590 595                                                     |      |
| TTC TTT GCA ACT ATG GAT ATC GAA AAG TGA TAT GAT AGT GTA AAC AGA | 1939 |
| Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg |      |
| 600 605 610                                                     |      |
| GAA AAA CTA TCA ACA TTC CTA AAA ACT ACT AAA TTA CTT TCT TCA GAT | 1987 |
| Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp |      |
| 615 620 625                                                     |      |
| TTC TGG ATT ATG ACT GCA CAA ATT CTA AAG AGA AAG AAT AAC ATA GTT | 2035 |
| Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn Ile Val |      |
| 630 635 640 645                                                 |      |
| ATC GAT TCG AAA AAC TTT AGA AAG AAA GAA ATG AAA GAT TAT TTT AGA | 2083 |
| Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr Phe Arg |      |
| 650 655 660                                                     |      |
| CAG AAA TTC CAG AAG ATT GCA CTT GAA GGA GGA CAA TAT CCA ACC TTA | 2131 |
| Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro Thr Leu |      |
| 665 670 675                                                     |      |
| TTC AGT GTT CTT GAA AAT GAA CAA AAT GAC TTA AAT GCA AAG AAA ACA | 2179 |
| Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys Lys Thr |      |
| 680 685 690                                                     |      |
| TTA ATT GTT GAA GCA AAG CAA AGA AAT TAT TTT AAG AAA GAT AAC TTA | 2227 |
| Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp Asn Leu |      |
| 695 700 705                                                     |      |
| CTT CAA CCA GTC ATT AAT ATT TGC CAA TAT AAT TAC ATT AAC TTT AAT | 2275 |
| Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn Phe Asn |      |
| 710 715 720 725                                                 |      |
| GGG AAG TTT TAT AAA CAA ACA AAA GGA ATT CCT CAA GGT CTT TGA GTT | 2323 |
| Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val |      |
| 730 735 740                                                     |      |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TCA TCA ATT TTG TCA TCA TTT TAT TAT GCA ACA TTA GAG GAA AGC TCC<br>Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser<br>745 750 755     | 2371 |
| TTA GGA TTC CTT AGA GAT GAA TCA ATG AAC CCT GAA AAT CCA AAT GTT<br>Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro Asn Val<br>760 765 770     | 2419 |
| AAT CTT CTA ATG AGA CTT ACA GAT GAC TAT CTT TTG ATT ACA ACT CAA<br>Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Ile Thr Thr Gln<br>775 780 785         | 2467 |
| GAG AAT AAT GCA GTA TTG TTT ATT GAG AAA CTT ATA AAC GTA AGT CGT<br>Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg<br>790 795 800 805 | 2515 |
| GAA AAT GGA TTT AAA TTC AAT ATG AAG AAA CTA CAG ACT AGT TTT CCA<br>Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro<br>810 815 820     | 2563 |
| TTA AGT CCA AGC AAA TTT GCA AAA TAC GGA ATG GAT AGT GTT GAG GAG<br>Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val Glu Glu<br>825 830 835     | 2611 |
| CAA AAT ATT GTT CAA GAT TAC TGC GAT TGG ATT GGC ATC TCA ATT GAT<br>Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser Ile Asp<br>840 845 850     | 2659 |
| ATG AAA ACT CTT GCT TTA ATG CCA AAT ATT AAC TTG AGA ATA GAA GGA<br>Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile Glu Gly<br>855 860 865     | 2707 |
| ATT CTG TGT ACA CTC AAT CTA AAC ATG CAA ACA AAG AAA GCA TCA ATG<br>Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala Ser Met<br>870 875 880 885 | 2755 |
| TGG CTC AAG AAG AAA CTA AAG TCG TTT TTA ATG AAT AAC ATT ACC CAT<br>Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile Thr His<br>890 895 900     | 2803 |
| TAT TTT AGA AAG ACG ATT ACA ACC GAA GAC TTT GCG AAT AAA ACT CTC<br>Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala Asn Lys Thr Leu<br>905 910 915     | 2851 |
| AAC AAG TTA TTT ATA TCA GGC GGT TAC AAA TAC ATG CAA TGA GCC AAA<br>Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys Ala Lys<br>920 925 930     | 2899 |
| GAA TAC AAG GAC CAC TTT AAG AAG AAC TTA GCT ATG AGC AGT ATG ATC<br>Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser Met Ile<br>935 940 945     | 2947 |
| GAC TTA GAG GTA TCT AAA ATT ATA TAC TCT GTA ACC AGA GCA TTC TTT<br>Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala Phe Phe<br>950 955 960 965 | 2995 |
| AAA TAC CTT GTG TGC AAT ATT AAG GAT ACA ATT TTT GGA GAG GAG CAT<br>Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu Glu His<br>970 975 980     | 3043 |

TAT CCA GAC TTT TTC CTT AGC ACA CTG AAG CAC TTT ATT GAA ATA TTC 3091  
 Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu Ile Phe  
           985                                  990                                  995

AGC ACA AAA AAG TAC ATT TTC AAC AGA GTT TGC ATG ATC CTC AAG GCA 3139  
 Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu Lys Ala  
           1000                                  1005                                  1010

AAA GAA GCA AAG CTA AAA AGT GAC CAA TGT CAA TCT CTA ATT CAA TAT 3187  
 Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile Gln Tyr  
           1015                                  1020                                  1025

GAT GCA TAGTCGACTA TTCTAACTTA TTTTGGAAG TTAATTTTCA ATTTTGTCT 3243  
 Asp Ala  
 1030

TATATACTGG GGTTTTGGGG TTTTGGGGTT TTGGGG 3279

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser  
   1                                  5                                  10                                  15

Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser  
           20                                  25                                  30

Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr  
           35                                  40                                  45

Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala  
           50                                  55                                  60

Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys  
   65                                  70                                  75                                  80

Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu  
           85                                  90                                  95

Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln  
           100                                  105                                  110

Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu  
           115                                  120                                  125

Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp  
           130                                  135                                  140

Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr  
   145                                  150                                  155                                  160

Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln  
 165 170 175  
 Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe  
 180 185 190  
 Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys  
 195 200 205  
 Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu  
 210 215 220  
 Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg  
 225 230 235 240  
 Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys  
 245 250 255  
 His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala  
 260 265 270  
 Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys  
 275 280 285  
 Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val  
 290 295 300  
 Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro  
 305 310 315 320  
 Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys  
 325 330 335  
 Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr  
 340 345 350  
 Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn  
 355 360 365  
 Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln  
 370 375 380  
 Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His  
 385 390 395 400  
 Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met  
 405 410 415  
 Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn  
 420 425 430  
 Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val  
 435 440 445  
 Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser  
 450 455 460  
 Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met  
 465 470 475 480

Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln  
 485 490 495  
 Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly  
 500 505 510  
 Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr  
 515 520 525  
 Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr  
 530 535 540  
 Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys  
 545 550 555 560  
 Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp  
 565 570 575  
 Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val  
 580 585 590  
 Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr  
 595 600 605  
 Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys  
 610 615 620  
 Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg  
 625 630 635 640  
 Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met  
 645 650 655  
 Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly  
 660 665 670  
 Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu  
 675 680 685  
 Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe  
 690 695 700  
 Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn  
 705 710 715 720  
 Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro  
 725 730 735  
 Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr  
 740 745 750  
 Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro  
 755 760 765  
 Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu  
 770 775 780  
 Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu  
 785 790 795 800

Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu  
 805 810 815  
 Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met  
 820 825 830  
 Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile  
 835 840 845  
 Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn  
 850 855 860  
 Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr  
 865 870 875 880  
 Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met  
 885 890 895  
 Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe  
 900 905 910  
 Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr  
 915 920 925  
 Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala  
 930 935 940  
 Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val  
 945 950 955 960  
 Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile  
 965 970 975  
 Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His  
 980 985 990  
 Phe Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys  
 995 1000 1005  
 Met Ile Leu Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln  
 1010 1015 1020  
 Ser Leu Ile Gln Tyr Asp Ala  
 1025 1030

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(959..1216, 1273..1353, 1425..1543,  
1595..1857, 1894..2286, 2326..2396, 2436..2705,  
2746..2862, 2914..3083, 3125..3309, 3356..3504,  
3546..3759, 3797..4046, 4086..4252, 4296..4392,  
4435..4597)(D) OTHER INFORMATION: /note= "Schizosaccharomyces pombe  
telomerase catalytic subunit (TRT)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

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GGTACCGATT TACTTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT 60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAAGT CAAATTCCAA TATGAAGGTG 120
TTATTAGTGA TCGATAATAT TTCTATTTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG 180
AACAACTTCC TTCCCCCTAA AGACTTTTAC TTTATTAATT TACTTTTCAA ATATATTTTCG 240
GGTTCGCTTA CTTTAAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGTG 300
TCTACCCCGT CATTGGATAT AGCTCTTGA GTAGCTCACA GAAATCCTTA CAAATCTTCT 360
GATGAGACTA TATTAGATTC ATTACAGTCC GTGCATATTC TTAACATGGA GCCTTACACT 420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTTG CCTTGAAAAG 480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGGTA ATCCGCGGAA GTTTTTTGAT 540
GCTTGACACAC GTCTAGCATG ATTGAGATAT TCAAAAATTT CTATCCACTA CAACTCCTTT 600
AACGCGGTTT TATTTTTCTA TTTTCTATTC TCATGTTGTT CCAAATATGT ATCATCTCGT 660
ATTAGGCTTT TTTCCGTTTT ACTCCTGGAA TCGTACCTTT TTCACTATTC CCCCTAATGA 720
ATAATCTAAA TTAGTTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG 780
TGTAATGTTA TTAGTTTAAA GATACTTTGC AAAACATTTA TTAGCTATCA TTATATAAAA 840
AAAATCCTAT AATTATAAAT ATTAATCAAT ATTTGCGGTC ACTATTTATT TAAACGTTA 900
TGATCAGTAG GACACTTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC 958
ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG 1006
Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu
 1 5 10 15

AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT 1054
Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val
 20 25 30

TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG 1102
Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu
 35 40 45

AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA 1150
Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val
 50 55 60

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|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA<br>Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro<br>65 70 75 80     | 1198 |
| AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGTTTTG ATTTTTTTCT<br>Lys Cys Ser Gln Ser Glu<br>85                                                             | 1246 |
| ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG<br>Leu Ile Ala Asn Val Val Lys Gln Met<br>90 95                                      | 1299 |
| TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT<br>Phe Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe<br>100 105 110     | 1347 |
| TCC ATG GTAAGGTATT CTAATTGTGA AATATTTACC TGCAATTACT GTTTCAAAGA<br>Ser Met                                                                             | 1403 |
| GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA<br>Asn His Glu Asp Phe Arg Ala Met His Val<br>115 120                                 | 1454 |
| AAC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA<br>Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile<br>125 130 135     | 1502 |
| TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT<br>Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Leu Glu Ile<br>140 145 150                      | 1543 |
| GTAAATACCG GTTAAGATGT TGCGCACTTT GAACAAGACT GACAAGTATA G T ATC<br>Ile                                                                                 | 1598 |
| GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG<br>Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu<br>155 160 165 170 | 1646 |
| GCT CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT<br>Ala Leu Pro Asn Asp Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe<br>175 180 185     | 1694 |
| AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC<br>Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr<br>190 195 200     | 1742 |
| ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC<br>Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser<br>205 210 215     | 1790 |
| TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC<br>Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser<br>220 225 230     | 1838 |
| TAT AAG AAG TTT AAG CAA G GTAACATAA CTGTTATCCT TCATAACTAA<br>Tyr Lys Lys Phe Lys Gln<br>235 240                                                       | 1887 |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TTTTAG AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA<br>Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr<br>245 250                   | 1934 |
| GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA<br>Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile<br>255 260 265 270 | 1982 |
| AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA<br>Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser<br>275 280 285     | 2030 |
| CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT<br>Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile<br>290 295 300     | 2078 |
| GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC<br>Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr<br>305 310 315     | 2126 |
| AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT<br>Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu<br>320 325 330     | 2174 |
| AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT<br>Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile<br>335 340 345 350 | 2222 |
| CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT<br>Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe<br>355 360 365     | 2270 |
| GAG ATA ATA TTA AAA G GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAG AC<br>2327<br>Glu Ile Ile Leu Lys<br>370                                             | Asp  |
| CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT<br>Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His<br>375 380 385     | 2375 |
| TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTTTT ACCATTAATT<br>Tyr Leu Met Ser Asn Ile Lys<br>390 395                                               | 2426 |
| AACAATCAG ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA<br>Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser<br>400 405                       | 2474 |
| AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT<br>Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe<br>410 415 420     | 2522 |
| GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA<br>Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu<br>425 430 435 440 | 2570 |
| CAA TCT TTT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT<br>Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr<br>445 450 455     | 2618 |

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|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT<br>Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile<br>460 465 470     | 2666 |
| ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTTAAA<br>Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu<br>475 480 485                  | 2715 |
| GTATTTTTTG CAAAAAGCTA ATATTTTCAG AAC AAT GTT AGG ATG GAT ACT CAG<br>Asn Asn Val Arg Met Asp Thr Gln<br>490                                            | 2769 |
| AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT<br>Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn<br>495 500 505     | 2817 |
| ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG<br>Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys<br>510 515 520             | 2862 |
| GTATTAATTT TTGGTCATCA ATGTACTTTA CTTCTAATCT ATTATTAGCA G ATG GGT<br>Met Gly<br>525                                                                    | 2919 |
| TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG<br>Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val<br>530 535 540     | 2967 |
| GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA<br>Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro<br>545 550 555     | 3015 |
| TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT<br>Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu<br>560 565 570     | 3063 |
| CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT<br>Leu Lys His Arg Met Phe Gly<br>575 580                                                 | 3113 |
| TAATTTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC<br>Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser<br>585 590                          | 3161 |
| TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG<br>Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys<br>595 600 605     | 3209 |
| AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT<br>Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His<br>610 615 620 625 | 3257 |
| GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC<br>Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser<br>630 635 640     | 3305 |
| TAT T GTAAGTTTAT TTTTTCATTG GAATTTTSTA ACAAATTCTT TTTTAG TT<br>Tyr Phe                                                                                | 3357 |

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|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA<br>Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr<br>645 650 655     | 3405 |
| TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT<br>Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser<br>660 665 670 675 | 3453 |
| TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT<br>Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val<br>680 685 690     | 3501 |
| AAG GTATACCAAT TGTGAATTG TAATAACACT AATGAACTA G ATA GGA AAT<br>Lys Ile Gly Asn<br>695                                                                 | 3554 |
| TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA<br>Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser<br>700 705 710     | 3602 |
| TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA<br>Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu<br>715 720 725     | 3650 |
| TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT<br>Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp<br>730 735 740     | 3698 |
| TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT<br>Phe Leu Phe Ile Thr Val Asn Lys Lys Asp Ala Lys Lys Phe Leu Asn<br>745 750 755     | 3746 |
| TTA TCT TTA AGA G GTGAGTTGCT GTCATTCCTA AGTTCTAACC GTTGAAG GA<br>Leu Ser Leu Arg Gly<br>760                                                           | 3798 |
| TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC<br>Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn<br>765 770 775 780 | 3846 |
| TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC<br>Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser<br>785 790 795     | 3894 |
| AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT<br>Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu<br>800 805 810     | 3942 |
| GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT<br>Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser<br>815 820 825     | 3990 |
| ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA<br>Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys<br>830 835 840     | 4038 |
| ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG<br>Ile Leu Arg Ser<br>845                                                                 | 4089 |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA<br>Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser<br>850 855 860     | 4137 |
| AAA TTC AAT TCT TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT<br>Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys<br>865 870 875 880 | 4185 |
| ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC<br>Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro<br>885 890 895     | 4233 |
| CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTTAACTA GAAAAGTCAT<br>Gln Arg Met Phe Ile Thr<br>900                                                          | 4282 |
| TAATTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA<br>Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys<br>905 910                           | 4330 |
| AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT<br>Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser<br>915 920 925 930 | 4378 |
| GCA GAA GTC AAA TG GTACGTGTCG GTCTCGAGAC TTCAGCAATA TTGACACATC<br>Ala Glu Val Lys Trp<br>935                                                          | 4432 |
| AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA<br>Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys<br>940 945 950        | 4480 |
| TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT<br>Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr<br>955 960 965     | 4528 |
| GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA<br>Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu<br>970 975 980     | 4576 |
| CAT AGA AGA ATA GCT GAT TAATGTCATT TTCAATTTAT TATATACATC<br>His Arg Arg Ile Ala Asp<br>985                                                            | 4624 |
| CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC                                                                                     | 4684 |
| ATACTATAGG ATTTCTAGTA AAGTAAAATT AATCTCGTTA TTAGTTTTGA TTGACTTGTC                                                                                     | 4744 |
| TTTATCCTTA TACTTTTAAAG AAAGATTGAC AGTGTTGCT GACTACTGCC CACATGCCCCA                                                                                    | 4804 |
| TTAAACGGGA GTGGTTAAAC ATTAAAAGTA ATACATGAGG CTAATCTCCT TTCATTTAGA                                                                                     | 4864 |
| ATAAGGAAAG TGTTTTTCTA TAATGAATAA TGCCCGCACT AATGCAAAAA GACGAAGATT                                                                                     | 4924 |
| ATCTTCTAAA CAAGGGGGAT TAAGCATATC CGAAGGAAAA GAGAGTAATA TACCCAGTGT                                                                                     | 4984 |
| TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTTGG                                                                                     | 5044 |
| TGACCGAATT TTGGTAAAAG CCCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACG                                                                                     | 5104 |
| AAAAGAACT AAGGATAGTT TGAATACTAA TAGCTCATTT AATGTCTTAT ATAAGGTTTT                                                                                      | 5164 |

GTTTTTTCCT GACTTCAATT TTGCATGGGT GAAAAGAAAT AGTGTTAAGC CATTATTGGA 5224  
 TTCCGAAATA GCCAAATTTC TTGGTTCCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC 5284  
 TTATGAGGCT TCAAAAATC CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT 5344  
 GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTTG CAAAAAAGAA AATATCATTG 5404  
 GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT 5464  
 AACTTCTATT TCTGAAATGT ATGGTCCTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA 5524  
 GTTAAGTGAC CAAAGGTACC 5544

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu  
 1 5 10 15  
 Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val  
 20 25 30  
 Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu  
 35 40 45  
 Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val  
 50 55 60  
 Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro  
 65 70 75 80  
 Lys Cys Ser Gln Ser Glu Leu Ile Ala Asn Val Val Lys Gln Met Phe  
 85 90 95  
 Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe Ser  
 100 105 110  
 Met Asn His Glu Asp Phe Arg Ala Met His Val Asn Gly Val Gln Asn  
 115 120 125  
 Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile Ser Ile Leu Glu Ser  
 130 135 140  
 Lys Asn Trp Gln Leu Leu Leu Glu Ile Ile Gly Ser Asp Ala Met His  
 145 150 155 160  
 Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu Ala Leu Pro Asn Asp Asn  
 165 170 175  
 Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe Lys Asn Asn Val Phe Glu  
 180 185 190

Glu Thr Val Ser Lys Lys Arg Lys Arg Thr Ile Glu Thr Ser Ile Thr  
 195 200 205  
 Gln Asn Lys Ser Ala Arg Lys Glu Val Ser Trp Asn Ser Ile Ser Ile  
 210 215 220  
 Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser Tyr Lys Lys Phe Lys Gln  
 225 230 235 240  
 Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr Val His  
 245 250 255  
 Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile Asn Ala  
 260 265 270  
 Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser Gln Ser  
 275 280 285  
 Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile Glu Gln  
 290 295 300  
 Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr Asn His  
 305 310 315 320  
 Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu Ser Tyr  
 325 330 335  
 Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile Leu Val  
 340 345 350  
 Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe Glu Ile  
 355 360 365  
 Ile Leu Lys Asp Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser  
 370 375 380  
 Phe Ser Leu His Tyr Leu Met Ser Asn Ile Lys Ile Ser Glu Ile Glu  
 385 390 395 400  
 Trp Leu Val Leu Gly Lys Arg Ser Asn Ala Lys Met Cys Leu Ser Asp  
 405 410 415  
 Phe Glu Lys Arg Lys Gln Ile Phe Ala Glu Phe Ile Tyr Trp Leu Tyr  
 420 425 430  
 Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu  
 435 440 445  
 Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys Asp Ile Trp  
 450 455 460  
 Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met Lys Met Glu Ala Phe  
 465 470 475 480  
 Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp Thr Gln Lys Thr Thr  
 485 490 495  
 Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg  
 500 505 510

Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys Met Gly Ser Asn  
 515 520 525  
 Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val Ala Ser  
 530 535 540  
 Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro Phe Asn  
 545 550 555 560  
 Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu Leu Lys  
 565 570 575  
 His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys  
 580 585 590  
 Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys  
 595 600 605  
 Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile  
 610 615 620  
 His Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe  
 625 630 635 640  
 Ser Tyr Phe Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser  
 645 650 655  
 Met Lys Thr Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr  
 660 665 670  
 Lys Ser Ser Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly  
 675 680 685  
 His Ile Val Lys Ile Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile  
 690 695 700  
 Pro Gln Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu  
 705 710 715 720  
 Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val  
 725 730 735  
 Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys Lys  
 740 745 750  
 Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His  
 755 760 765  
 Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn Ser  
 770 775 780  
 Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser Lys Lys Arg Met  
 785 790 795 800  
 Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu Asp Thr Leu Leu  
 805 810 815  
 Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser Thr Ser Val Glu  
 820 825 830



Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys Ile Leu Arg Ser  
835 840 845

Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser  
850 855 860

Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys  
865 870 875 880

Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro  
885 890 895

Gln Arg Met Phe Ile Thr Asp Leu Leu Asn Val Ile Gly Arg Lys Ile  
900 905 910

Trp Lys Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu  
915 920 925

Ser Ser Ala Glu Val Lys Trp Leu Phe Cys Leu Gly Met Arg Asp Gly  
930 935 940

Leu Lys Pro Ser Phe Lys Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr  
945 950 955 960

Gln Phe Gln Ser Leu Thr Asp Leu Ile Lys Pro Leu Arg Pro Val Leu  
965 970 975

Arg Gln Val Leu Phe Leu His Arg Arg Ile Ala Asp  
980 985

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GGGGTTTTGG GGTTTT

16

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1762
- (D) OTHER INFORMATION: /note= "gene encoding the 43 kDa telomerase protein subunit from *Euplotes aediculatus*"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```

CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG GTAGTTTAGA 60
AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA TTTGGATGAT ATAGAAAATT 120
TACTTCCTAA TACATTCAAC AAGTATAGCA GCTCTTGTAG TGACAAGAAA GGATGCAAAA 180
CATTGAAATC TGGCTCGAAA TCGCCTTCAT TGA CTATTCC AAAGTTGCAA AAACAATTAG 240
AGTTCTACTT CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA 300
AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA AATCAGGTAA 360
TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA TTATGGAGAA AATTACTTAA 420
TACTAAAAGG TAAACAGTTT GGATTATTTT CCTAGCCAAC AATGATGAGT ATATTAAATT 480
CATATGAGAA TGAGTCAAAG GATCTCGATA CATCAGACTT ACCAAGACA AACTCGCTAT 540
AAAACGCAAG AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTA CTATTTCG 600
TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC TTGAGACAAT 660
TGAAAAAGCT GTTTACA ACT GAAGGAATCG CAGTTCTGAA AGTTCTGATG TGTATGCCAT 720
TATTTTGTGA ATTAATCTCA AATATCTTAT CTCAATTTAA TGGATAGCTA TAGAAACAAA 780
CCAAATAAAC CATGCAAGTT TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC 840
TGAATTTATA TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC 900
TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT AAAAGAAGCA 960
GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAT TTGTTGATTC TTCTGTAACC 1020
GGAATTAACA ACAAGAATAT TAGCAACGAA AAAGAAGAAG AGCTATCACA ATCCTGATTC 1080
TTAAAGATTT CAAAATTCC AGGTAAGAGA GATACATTCA TTAAATTCA TATATTATAG 1140
TTTTTCATTT CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA 1200

```

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT TCACATTCAT | 1260 |
| AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA GCAGTCATCC GTTTTAAAAA | 1320 |
| TAGTGCTATG AGGACTAAAT TTTTAGAGTC AAGAAATGGA GCCGAAATCT TAATCAAAAA | 1380 |
| GAATTGCGTC GATATTGCAA AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA | 1440 |
| ATCTTGATTG ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA  | 1500 |
| GTAACCTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG CGATCTTCAA | 1560 |
| TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA ATACAAACCT TGGTCAAAAT | 1620 |
| ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA AAAGAAAAAA TAAGGCAATA AATAAAATGA | 1680 |
| GTACAGAAGT GAAGAAATAA AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT  | 1740 |
| TTGGGGTTTT GGGGTTTTGG GG                                          | 1762 |

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

|     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gln | Asn | Pro | Lys | Thr | Pro | Lys | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Lys | Lys | Leu | Arg |
| 1   |     |     |     | 5   |     |

## (2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe Arg Asn Lys Ile Leu Phe Pro His Lys Trp Arg Trp Ile Leu Ile  
 1                    5                    10                    15  
 Trp Met Ile

## (2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 41 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Lys Ile Tyr Phe Leu Ile His Ser Thr Ser Ile Ala Ala Leu Val Val  
 1                    5                    10                    15  
 Thr Arg Lys Asp Ala Lys His Cys Asn Leu Ala Arg Asn Arg Leu His  
 20                    25                    30  
 Cys Leu Phe Gln Ser Cys Lys Asn Asn  
 35                    40

## (2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Ser Ser Thr Ser Arg Met Gln Ile Phe Ile Thr Ile Leu Ser Cys Glu  
 1                    5                    10                    15  
 Asn

## (2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Lys Ala Glu Ser Lys Glu  
1 5

## (2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Lys Leu Lys His Tyr  
1 5

## (2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Cys Leu Asn Lys Ile Arg  
1 5

## (2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Cys Gly Leu Phe Tyr Phe Leu Asp His Phe Leu Arg Ser Ile Met Glu  
 1 5 10 15

Lys Ile Thr

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Lys Val Asn Ser Leu Asp Tyr Phe Pro Ser Gln Gln Cys Cys Val Tyr  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Ile His Met Arg Met Ser Gln Arg Ile Ser Ile His Gln Thr Tyr Gln  
 1 5 10 15

Arg Gln Thr Arg Tyr Lys Thr Gln Glu Lys Val Cys  
 20 25

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ser Asn Ser Arg Arg Thr Tyr Cys Ile Tyr Tyr Ser Tyr Gly Phe Tyr  
 1 5 10 15

Tyr Asn Cys Phe Arg Tyr Arg Arg Cys Thr Pro Glu Ser Cys Asp Asn  
                   20                  25                  30  
 Cys Lys Ser Cys Leu Gln Leu Lys Glu Ser Gln Phe Cys Lys Phe Cys  
                   35                  40                  45  
 Cys Val Cys His Tyr Phe Val Asn  
                   50                  55

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Ser Gln Ile Ser Tyr Leu Asn Leu Met Asp Ser Tyr Arg Asn Lys Pro  
 1                  5                  10                  15  
 Asn Lys Pro Cys- Lys Phe Asn Gly Ile Tyr Val Lys Ser Phe Gly Thr  
                   20                  25                  30  
 Asn Ala His Cys Ile Tyr Ile Gly Phe Leu Lys His Arg Tyr Thr Glu  
                   35                  40                  45  
 Cys Phe Arg Asp Cys Phe Ser Leu Gln Gln Ile Thr Cys Phe Asp Tyr  
                   50                  55                  60  
 Ser Cys Ser Ser Leu Ile Ser Leu Lys Glu Ala Gly Glu Met Lys Arg  
                   65                  70                  75                  80  
 Arg Leu Lys Lys Glu Ile Ser Lys Phe Val Asp Ser Ser Val Thr Gly  
                   85                  90                  95  
 Ile Asn Asn Lys Asn Ile Ser Asn Glu Lys Glu Glu Glu Leu Ser Gln  
                   100                  105                  110  
 Ser Cys Phe Leu Lys Ile Ser Lys Ile Pro Gly Lys Arg Asp Thr Phe  
                   115                  120                  125  
 Ile Lys Ile His Ile Leu  
                   130

## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

Phe Phe Ile Ser Gln Leu Leu Phe Ser Phe Ile Leu Thr Ile Phe Phe  
1 5 10 15  
Asp

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Leu Ile His Ile His Arg Ser Thr Phe Ile Tyr Pro Ile Arg Cys  
1                   5                   10                   15



## (2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Gly Asn Ser Ser His Pro Phe  
 1 5

## (2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Cys Tyr Glu Asp  
 1

## (2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ile Phe Arg Val Lys Lys Trp Ser Arg Asn Leu Asn Gln Lys Glu Leu  
 1 5 10 15  
 Arg Arg Tyr Cys Lys Arg Ile Glu Leu  
 20 25

## (2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Val Leu Pro Ile Leu Ile Asp Cys Arg Asp Cys Arg Gly Asn Cys Thr  
1 5 10 15

Glu Asp His

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Arg Asn Lys Val Thr Phe Ile Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Ile Thr Asn Ile Glu Ile Ser Asp Leu Gln Leu Thr Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Thr Ile Lys Asn Thr Asn Leu Gly Gln Asn Ile Glu Glu Gly Lys Glu  
1 5 10 15

Asp Gln Leu Ala Lys Glu Lys Ile Arg Gln  
 20 25

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ile Lys Cys Val Gln Lys Cys Arg Asn Lys Arg Phe Ile Phe Phe Asn  
 1 5 10 15  
 Asn Leu Leu Lys Arg Gly Val Leu Gly Phe Trp Gly Phe Gly  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Pro Lys Thr Pro Lys Pro Gln Asn Pro Tyr Lys Lys Arg Lys Asn Cys  
 1 5 10 15  
 Gly Ser Leu Glu Ile Lys Tyr Tyr Ser Arg Thr Asn Gly Asp Gly Tyr  
 20 25 30  
 Cys Phe Gly Cys Tyr Arg Lys Phe Thr Ser  
 35 40

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Tyr Ile Gln Gln Val  
1 5

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Cys Gln Glu Arg Met Gln Asn Ile Glu Ile Trp Leu Glu Ile Ala Phe  
1 5 10 15

Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg Val Leu Leu Leu Gly  
20 25 30

Cys Lys Ser Leu  
35

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Arg Phe Phe Leu Glu Lys Ile Ser Phe Lys Lys Arg Arg Ala Lys Ser  
1 5 10 15

Arg Asn Cys Asn Ile Thr Asn Val  
20

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Ile Lys Ser Gly Asn Glu Asp Tyr Ser Ile Phe  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Gly Ala Leu Trp Arg Lys Leu Leu Asn Thr Lys Arg  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids -
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Thr Val Trp Ile Ile Ser Leu Ala Asn Asn Asp Glu Tyr Ile Lys Phe  
 1 5 10 15

Ile Cys Glu Cys Val Lys Gly Ser Arg Tyr Ile Arg Leu Thr Lys Asp  
 20 25 30

Lys Leu Ala Ile Lys Arg Lys Lys Lys Phe Asp Asn Arg Thr Ala Glu  
 35 40 45

Glu Leu Ile Ala Phe Thr Ile Arg Met Gly Phe Ile Thr Ile Val Leu  
 50 55 60

Gly Ile Asp Gly Glu Leu Pro Ser Leu Glu Thr Ile Glu Lys Ala Val  
 65 70 75 80

Tyr Asn Cys Arg Asn Arg Ser Ser Glu Ser Ser Asp Val Tyr Ala Ile  
 85 90 95

Ile Leu Cys Ile Asn Leu Lys Tyr Leu Ile Ser Ile  
 100 105

## (2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Trp Ile Ala Ile Glu Thr Asn Gln Ile Asn His Ala Ser Leu Met Glu  
 1                   5                   10                   15

Tyr Thr Leu Asn Pro Leu Gly Gln Met His Thr Glu Phe Ile Leu Asp  
           20                   25                   30

Ser

## (2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Ser Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu Ala Tyr Asn Arg  
 1                   5                   10                   15

Leu Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr Leu  
           20                   25

## (2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Lys Lys Gln Ala Lys Cys Lys Glu Asp  
 1                   5

## (2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Arg Lys Arg Phe Gln Asn Leu Leu Ile Leu Leu  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys Lys Lys Ser Tyr  
 1                      5                      10                      15

His Asn Pro Asp Ser  
 20

## (2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Arg Phe Gln Lys Phe Gln Val Arg Glu Ile His Ser Leu Lys Phe Ile  
 1                      5                      10                      15

Tyr Tyr Ser Phe Ser Phe His Ser Cys Tyr Phe Leu Leu Ser  
 20                      25                      30

## (2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Gln Tyr Phe Leu Ile Ser Trp Lys  
 1 5

## (2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg  
 1 5 10

## (2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Leu Ser Leu Phe Thr Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp  
 1 5 10 15

Asp Lys Glu Thr Ala Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr  
 20 25 30

Lys Phe Leu Glu Ser Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn  
 35 40 45

Cys Val Asp Ile Ala Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys  
 50 55 60

Tyr Tyr Gln Ser Cys Leu Ile Glu Glu Ile Asp Glu Ala Thr Ala Gln  
 65 70 75 80



Lys Ile Ile Lys Glu Ile Lys  
85

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Leu Leu Leu Ile Arg Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Thr Lys Leu Leu Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Arg Ser Ala Ile Phe Asn Cys Arg Asn Lys Ser Cys Thr Lys Val Arg  
1 5 10 15

Gln

## (2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Lys Ile Gln Thr Leu Val Lys Ile Leu Arg Lys Glu Lys Lys Thr Ser  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Gln Lys Lys Lys  
 1

## (2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Asn Glu Tyr Arg Ser Glu Glu Ile Lys Asp Leu Phe Phe Ser Ile Ile  
 1                      5                      10                      15

Tyr Cys Lys Glu Gly Phe Trp Gly Phe Gly Val Leu Gly  
 20                      25

## (2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Pro Lys Pro Gln Asn Pro Lys Thr Pro Ile Lys Lys Glu Lys Ile Glu  
1                   5                   10                   15  
Val Val

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Asn Ile Ile Pro Ala Gln Met Glu Met Asp Ile Asp Leu Asp Asp Ile  
1                   5                   10                   15  
Glu Asn Leu Leu Pro Asn Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser  
20                   25                   30  
Asp Lys Lys Gly Cys Lys Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser  
35                   40                   45  
Leu Thr Ile Pro Lys Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp  
50                   55                   60  
Ala Asn Leu Tyr Asn Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser  
65                   70                   75                   80  
Gly Glu Gln Arg Val Glu Ile Glu Thr Leu Leu Met Phe Lys  
85                   90

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Asn Gln Val Met Arg Ile Ile Leu Phe Phe Arg Ser Leu Leu Lys Glu  
1                   5                   10                   15

Phe Pro

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Asn Ala Arg Lys Ser Leu Ile Ile Glu Gln Gln Lys Asn Leu Leu His  
1 5 10 15

Leu Leu Phe Val Trp Val Leu Leu Gln Leu Phe  
20 25

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Val Ser Thr Val Asn Ser Arg Val Leu Arg Gln Leu Lys Lys Leu Phe  
1 5 10 15

Thr Thr Glu Gly Ile Ala Val Leu Lys Val Leu Met Cys Met Pro Leu  
                   20                  25                  30

Phe Cys Glu Leu Ile Ser Asn Ile Leu Ser Gln Phe Asn Gly  
           35                  40                  45

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Lys Gln Thr Lys  
 1

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Thr Met Gln Val  
 1

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Trp Asn Ile Arg  
 1

## (2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Ile Leu Trp Asp Lys Cys Thr Leu Asn Leu Tyr Trp Ile Leu Lys Ala  
 1                    5                    10                    15

## (2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Ile His Arg Met Leu  
 1                    5

## (2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Leu Thr Thr Asp Tyr Leu Phe Cys Leu Leu Leu Ile Ser Tyr Ile  
 1                    5                    10                    15

Phe Lys Arg Ser Arg Arg Asn Glu Lys Lys Thr Lys Glu Arg Asp Phe  
 20                    25                    30

Lys Ile Cys Cys Phe Phe Cys Asn Arg Asn  
 35                    40

## (2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Gln Gln Glu Tyr  
1

## (2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Gln Arg Lys Arg Arg Arg Ala Ile Thr Ile Leu Ile Leu Lys Asp Phe  
1                      5                      10                      15  
  
Lys Asn Ser Arg  
20

## (2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Glu Arg Tyr Ile His  
1                      5

## (2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Asn Ser Tyr Ile Ile Val Phe His Phe Thr Ala Val Ile Phe Phe Tyr
1 5 10 15
Leu Asn Asn Ile Phe Cys Leu Ala Gly Ser Lys Lys Tyr Gln Ile Arg
 20 25 30
Glu Ala Leu Asp Cys Gly Asn Leu Ala Tyr Ser His Ser
 35 40 45

```

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

Ile Asp Leu His Ile Ser Asn Thr Met Ile Arg Lys Gln Gln Ser Ser
1 5 10 15
Val Leu Lys Ile Val Leu Cys Gly Leu Asn Phe
 20 25

```

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

Ser Gln Glu Met Glu Pro Lys Ser
1 5

```

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Ser Lys Arg Ile Ala Ser Ile Leu Gln Lys Asn Arg Thr Leu Asn Leu  
1 5 10 15

Ser Leu Ile Ser Ile Thr Asn Leu Asp Cys Leu Lys Arg Leu Thr Arg  
20 25 30

Gln Leu His Arg Arg Ser Leu Lys Lys  
35 40

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Ser Asn Phe Tyr  
1

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Leu Glu Asn Lys Leu Asn Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Tyr Arg Asp Gln Arg Ser Ser Ile Asp Glu Ile Lys Ala Glu Leu Lys  
1 5 10 15

Leu Asp Asn Lys Lys Tyr Lys Pro Trp Ser Lys Tyr Cys Gly Arg Lys  
 20 25 30

Arg Arg Pro Val Ser Lys Arg Lys Asn Lys Ala Ile Asn Lys Met Ser  
 35 40 45

Thr Glu Val Lys Lys  
 50

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Lys Ile Tyr Phe Phe Gln  
 1 5

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Phe Ile Glu Lys Arg Gly Phe Gly Val Leu Gly Phe Trp  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1007 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala  
 1 5 10 15

Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp  
 20 25 30  
 Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys  
 35 40 45  
 Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr  
 50 55 60  
 Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu  
 65 70 75 80  
 Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val  
 85 90 95  
 Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys  
 100 105 110  
 Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu  
 115 120 125  
 Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn  
 130 135 140  
 Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr  
 145 150 155 160  
 Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe  
 165 170 175  
 Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp  
 180 185 190  
 Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys  
 195 200 205  
 Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn  
 210 215 220  
 Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile  
 225 230 235 240  
 Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His  
 245 250 255  
 Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln  
 260 265 270  
 Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu  
 275 280 285  
 Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys  
 290 295 300  
 Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu  
 305 310 315 320  
 Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr  
 325 330 335

Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr  
 340 345 350  
 Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile  
 355 360 365  
 Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys  
 370 375 380  
 Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys  
 385 390 395 400  
 Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln  
 405 410 415  
 Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile  
 420 425 430  
 Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val  
 435 440 445  
 Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr  
 450 455 460  
 Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys  
 465 470 475 480  
 Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu  
 485 490 495  
 Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys  
 500 505 510  
 Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe  
 515 520 525  
 Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr  
 530 535 540  
 Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn  
 545 550 555 560  
 Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp  
 565 570 575  
 Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly  
 580 585 590  
 Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp  
 595 600 605  
 Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu  
 610 615 620  
 Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys  
 625 630 635 640  
 Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys  
 645 650 655

Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln  
 660 665 670  
 Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn  
 675 680 685  
 Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys  
 690 695 700  
 Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr  
 705 710 715 720  
 Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln  
 725 730 735  
 Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu  
 740 745 750  
 Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu  
 755 760 765  
 Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu  
 770 775 780  
 Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile  
 785 790 795 800  
 Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln  
 805 810 815  
 Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp  
 820 825 830  
 Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly  
 835 840 845  
 Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu  
 850 855 860  
 Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys  
 865 870 875 880  
 Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn  
 885 890 895  
 Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala  
 900 905 910  
 Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met  
 915 920 925  
 Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met  
 930 935 940  
 Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr  
 945 950 955 960  
 Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe  
 965 970 975

Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe  
                   980                                  985                                  990

Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys  
                   995                                  1000                                  1005

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Glu Leu Glu Leu Glu Met Gln Glu Asn Gln Asn Asp Ile Gln Val Arg  
 1                  5                                  10                                  15

Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr Ala Ala  
                   20                                  25                                  30

Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu Arg Arg  
                   35                                  40                                  45

Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp Pro Glu  
                   50                                  55                                  60

Phe Ile Cys Gln Leu Ala Val Tyr Ile Arg Asn Glu Leu Tyr Ile Arg  
                   65                                  70                                  75                                  80

Thr Thr Thr Asn Tyr Ile Val Ala Phe Cys Val Val His Lys Asn Thr  
                   85                                  90                                  95

Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu Pro Asn  
                   100                                  105                                  110

Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp  
                   115                                  120                                  125

Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp  
                   130                                  135                                  140

Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys Val Arg  
                   145                                  150                                  155                                  160

Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr Cys Thr  
                   165                                  170                                  175

Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val Thr Asn  
                   180                                  185                                  190

Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn Leu Leu  
                   195                                  200                                  205

Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys Arg Glu  
                   210                                  215                                  220

Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro  
 225 230 235 240  
 Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His  
 245 250 255  
 Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu  
 260 265 270  
 Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu  
 275 280 285  
 Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu Glu Glu  
 290 295 300  
 Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu  
 305 310 315 320  
 Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn  
 325 330 335  
 Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile  
 340 345 350  
 Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn  
 355 360 365  
 Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val Ile Asn  
 370 375 380  
 Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu  
 385 390 395 400  
 Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly  
 405 410 415  
 Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu  
 420 425 430  
 Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met  
 435 440 445  
 Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly  
 450 455 460  
 Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala  
 465 470 475 480  
 Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser  
 485 490 495  
 Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys  
 500 505 510  
 Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu  
 515 520 525  
 Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser  
 530 535 540

Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly  
 545 550 555 560  
 Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys  
 565 570 575  
 Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr  
 580 585 590  
 Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp Met Met  
 595 600 605  
 Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val  
 610 615 620  
 Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile  
 625 630 635 640  
 Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp  
 645 650 655  
 Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser  
 660 665 670  
 Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu  
 675 680 685  
 Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly  
 690 695

## (2) INFORMATION FOR SEQ ID NO:189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn Gln Val  
 1 5 10 15  
 Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr Lys Tyr  
 20 25 30  
 Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe Cys Gly  
 35 40 45  
 Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp Lys Lys  
 50 55 60  
 Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys Ser Thr  
 65 70 75 80  
 Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn Asn Ile  
 85 90 95



Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile Phe Tyr  
 100 105 110  
 Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His Glu Phe  
 115 120 125  
 Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln Thr Ile  
 130 135 140  
 Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu Lys Asp  
 145 150 155 160  
 Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys Asp Phe  
 165 170 175  
 Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu Asn Trp  
 180 185 190  
 Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr Arg Glu  
 195 200 205  
 Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr Asp Asn  
 210 215 220  
 Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile Leu Pro  
 225 230 235 240  
 Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys Lys Val  
 245 250 255  
 Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys Asn Leu  
 260 265 270  
 Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln Val Glu  
 275 280 285  
 Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val  
 290 295 300  
 Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val Ser Leu  
 305 310 315 320  
 Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys  
 325 330 335  
 Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser  
 340 345 350  
 Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu  
 355 360 365  
 Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg  
 370 375 380  
 Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys  
 385 390 395 400  
 Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr  
 405 410 415

Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met  
 420 425 430  
 Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met  
 435 440 445  
 Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro  
 450 455 460  
 Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val  
 465 470 475 480  
 Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser  
 485 490 495  
 Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg Lys Asn Asn  
 500 505 510  
 Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met Lys Asp Tyr  
 515 520 525  
 Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly Gln Tyr Pro  
 530 535 540  
 Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu Asn Ala Lys  
 545 550 555 560  
 Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe Lys Lys Asp  
 565 570 575  
 Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn Tyr Ile Asn  
 580 585 590  
 Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu  
 595 600 605  
 Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu  
 610 615 620  
 Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn Pro  
 625 630 635 640  
 Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr  
 645 650 655  
 Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val  
 660 665 670  
 Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser  
 675 680 685  
 Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met Asp Ser Val  
 690 695 700  
 Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile Gly Ile Ser  
 705 710 715 720  
 Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn Leu Arg Ile  
 725 730 735

Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys Lys Ala  
 740 745 750  
 Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn Asn Ile  
 755 760 765  
 Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala Asn Lys  
 770 775 780  
 Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met Gln Cys  
 785 790 795 800  
 Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met Ser Ser  
 805 810 815  
 Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr Arg Ala  
 820 825 830  
 Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe Gly Glu  
 835 840 845  
 Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe Ile Glu  
 850 855 860  
 Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys Met Ile Leu  
 865 870 875 880  
 Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln Ser Leu Ile  
 885 890 895  
 Gln

## (2) INFORMATION FOR SEQ ID NO:190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu  
 1 5 10 15  
 Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln  
 20 25 30  
 Ile Glu His Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu  
 35 40 45  
 Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn  
 50 55 60  
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu  
 65 70 75 80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Val | Asn | Gln | Ile | Lys | Gln | Gln | Val | Gln | Leu | Ile | Lys | Lys | Val | 85  | 90  | 95  |
| Gly | Ser | Lys | Val | Glu | Lys | Asp | Leu | Asn | Leu | Asn | Glu | Asp | Glu | Asn | Lys | 100 | 105 | 110 |
| Lys | Asn | Gly | Leu | Ser | Glu | Gln | Gln | Val | Lys | Glu | Glu | Gln | Leu | Arg | Thr | 115 | 120 | 125 |
| Ile | Thr | Glu | Glu | Gln | Val | Lys | Tyr | Gln | Asn | Leu | Val | Phe | Asn | Met | Asp | 130 | 135 | 140 |
| Tyr | Gln | Leu | Asp | Leu | Asn | Glu | Ser | Gly | Gly | His | Arg | Arg | His | Arg | Arg | 145 | 150 | 155 |
| Glu | Thr | Asp | Tyr | Asp | Thr | Glu | Lys | Trp | Phe | Glu | Ile | Ser | His | Asp | Gln | 165 | 170 | 175 |
| Lys | Asn | Tyr | Val | Ser | Ile | Tyr | Ala | Asn | Gln | Lys | Thr | Ser | Tyr | Cys | Trp | 180 | 185 | 190 |
| Trp | Leu | Lys | Asp | Tyr | Phe | Asn | Lys | Asn | Asn | Tyr | Asp | His | Leu | Asn | Val | 195 | 200 | 205 |
| Ser | Ile | Asn | Arg | Leu | Glu | Thr | Glu | Ala | Glu | Phe | Tyr | Ala | Phe | Asp | Asp | 210 | 215 | 220 |
| Phe | Ser | Gln | Thr | Ile | Lys | Leu | Thr | Asn | Asn | Ser | Tyr | Gln | Thr | Val | Asn | 225 | 230 | 235 |
| Ile | Asp | Val | Asn | Phe | Asp | Asn | Asn | Leu | Cys | Ile | Leu | Ala | Leu | Leu | Arg | 245 | 250 | 255 |
| Phe | Leu | Leu | Ser | Leu | Glu | Arg | Phe | Asn | Ile | Leu | Asn | Ile | Arg | Ser | Ser | 260 | 265 | 270 |
| Tyr | Thr | Arg | Asn | Gln | Tyr | Asn | Phe | Glu | Lys | Ile | Gly | Glu | Leu | Leu | Glu | 275 | 280 | 285 |
| Thr | Ile | Phe | Ala | Val | Val | Phe | Ser | His | Arg | His | Leu | Gln | Gly | Ile | His | 290 | 295 | 300 |
| Leu | Gln | Val | Pro | Cys | Glu | Ala | Phe | Gln | Tyr | Leu | Val | Asn | Ser | Ser | Ser | 305 | 310 | 315 |
| Gln | Ile | Ser | Val | Lys | Asp | Ser | Gln | Leu | Gln | Val | Tyr | Ser | Phe | Ser | Thr | 325 | 330 | 335 |
| Asp | Leu | Lys | Leu | Val | Asp | Thr | Asn | Lys | Val | Gln | Asp | Tyr | Phe | Lys | Phe | 340 | 345 | 350 |
| Leu | Gln | Glu | Phe | Pro | Arg | Leu | Thr | His | Val | Ser | Gln | Gln | Ala | Ile | Pro | 355 | 360 | 365 |
| Val | Ser | Ala | Thr | Asn | Ala | Val | Glu | Asn | Leu | Asn | Val | Leu | Leu | Lys | Lys | 370 | 375 | 380 |
| Val | Lys | His | Ala | Asn | Leu | Asn | Leu | Val | Ser | Ile | Pro | Thr | Gln | Phe | Asn | 385 | 390 | 395 |

Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly  
 405 410 415  
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu  
 420 425 430  
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr  
 435 440 445  
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala  
 450 455 460  
 Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro  
 465 470 475 480  
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe  
 485 490 495  
 Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn  
 500 505 510  
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile  
 515 520 525  
 Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met  
 530 535 540  
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu  
 545 550 555 560  
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His  
 565 570 575  
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys  
 580 585 590  
 Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe  
 595 600 605  
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu  
 610 615 620  
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser  
 625 630 635 640  
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu  
 645 650 655  
 Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu  
 660 665 670  
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser  
 675 680 685  
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe  
 690 695 700  
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr  
 705 710 715 720

Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln  
 725 730 735  
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu  
 740 745 750  
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln  
 755 760 765  
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln  
 770 775 780  
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser  
 785 790 795 800  
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr  
 805 810 815  
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn  
 820 825 830  
 Glu Glu Ile Gln Glu Leu Leu-Lys  
 835 840

## (2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 83 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn  
 1 5 10 15  
 Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys  
 20 25 30  
 Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln  
 35 40 45  
 Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu  
 50 55 60  
 Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr  
 65 70 75 80  
 Leu Leu Met

## (2) INFORMATION FOR SEQ ID NO:192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

```

Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser Leu Glu Ser Leu Glu
1 5 10 15
Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser Cys Lys Asn Leu Gln
20 25 30
Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro Asn Asn Ile Gln Lys
35 40 45
Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe Lys Gln Phe Glu Gln
50 55 60
Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys Ile Leu Asp Gln His
65 70 75 80
Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys Asn Lys Lys Ile Lys
85 90 95
Ala Phe Ile Leu
100

```

## (2) INFORMATION FOR SEQ ID NO:193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

Met Glu Met Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn
1 5 10 15
Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys
20 25 30
Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu
35 40 45
Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp
50 55 60

```

Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu  
 65 70 75 80

Ile Glu Thr Leu Leu  
 85

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu Asp Glu Ile  
 1 5 10 15

Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser Met Ser Thr  
 20 25 30

Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu  
 35 40 45

Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg Cys Glu Lys  
 50 55 60

Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys  
 65 70 75 80

Tyr Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro Ser Met Gln  
 85 90 95

Lys Leu Leu

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif A"



## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

INFORMATION FOR SEQ ID NO:197:-

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (ix) FEATURE:

- (ix) FEATURE:

- (ix) FEATURE:

- (A) NAME/KEY: Modified=site  
(B) LOCATION: 8..10  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Xaa Xaa Xaa Tyr Xaa Asp Asp Xaa Xaa Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..8  
(D) OTHER INFORMATION: /note= "consensus telomerase RT sequence  
from motif D"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 2  
(C) OTHER INFORMATION: /product= "OTHER".  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 4  
(C) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Gly Xaa Xaa Xaa Xaa Xaa Xaa Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..8
- (D) OTHER INFORMATION: /note= "consensus telomerase RT sequence from motif E"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe, Trp or Met"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Xaa Xaa Xaa Leu Gly Xaa Xaa Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from Dong (LINE)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Lys Asn Arg Asn Leu His Cys Thr Tyr Ile Asp Tyr Lys Lys Ala Phe  
 1                      5                      10                      15  
 Asp Ser Ile Pro His Ser Trp Leu Ile Gln Val Leu Glu Ile Tyr Lys  
                     20                      25                      30  
 Ile Asn

## (2) INFORMATION FOR SEQ ID NO:201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note="motif B peptide from  
Dong (LINE)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Arg Gln Ile Ala Ile Lys Lys Gly Ile Tyr Gln Gly Asp Ser Leu Ser  
 1                      5                      10                      15  
 Pro Leu Trp Phe Cys Leu Ala Leu Asn Pro Leu Ser His Gln Leu His  
                     20                      25                      30  
 Asn Asp Arg  
                     35

## (2) INFORMATION FOR SEQ ID NO:202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note="motif C and D peptide from  
Dong (LINE)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

His Leu Ile Tyr Met Asp Asp Ile Lys Leu Tyr Ala Lys Asn Asp Lys  
 1                      5                      10                      15  
 Glu Met Lys Lys Leu Ile Asp Thr Thr Thr Ile Phe Ser Asn Asp Ile  
                     20                      25                      30  
 Ser Met Gln Phe Gly Leu Asp Lys Cys Lys Thr  
                     35                      40

## (2) INFORMATION FOR SEQ ID NO:203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from  
Dong (LINE)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Lys Cys Leu Tyr Lys Tyr Leu Gly Phe Gln Gln  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae cytochrome  
oxidase group II intron 1-encoded  
mitochondrial protein"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Phe Gly Gly Ser Asn Trp Phe Arg Glu Val Asp Leu Lys Lys Cys Phe  
 1                      5                      10                      15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile  
                   20                                  25                                  30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B peptide from  
 Saccharomyces cerevisiae cytochrome  
 oxidase group II intron 1-encoded  
 mitochondrial protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

His Val Pro Val Gly Pro Arg Val Cys Val Gln Gly Ala Pro Thr Ser  
   1                  5                                  10                                  15

Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu Asp Arg Arg Leu Ala  
                   20                                  25                                  30

Gly Leu Ala  
           35

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "motif D peptide from  
 Saccharomyces cerevisiae cytochrome  
 oxidase group II intron 1-encoded  
 mitochondrial protein"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Lys Ile Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly Leu  
 1                      5                      10                      15  
 Thr Ile Asn Glu Glu Lys Thr Leu Ile  
                     20                      25

## (2) INFORMATION FOR SEQ ID NO:207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif A peptide from HIV RT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr  
 1                      5                      10                      15  
 Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr  
                     20                      25                      30  
 Ile Pro

## (2) INFORMATION FOR SEQ ID NO:208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif B peptide from HIV RT"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser  
 1                      5                      10                      15  
 Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg  
                     20                      25                      30



Lys Gln Asn  
35

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..17  
 (D) OTHER INFORMATION: /note= "motif C peptide from HIV RT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser His Leu Glu Ile  
 1                      5                      10                      15  
 Gly

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..37  
 (D) OTHER INFORMATION: /note= "motif D and E peptide from HIV RT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly  
 1                      5                      10                      15  
 Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp  
 20                      25                      30  
 Met Gly Tyr Glu Leu  
 35

## (2) INFORMATION FOR SEQ ID NO:211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: /note= "motif C and D peptide from  
Saccharomyces cerevisiae  
ESTp (L8543.12)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln  
1                      5                      10                      15

Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr  
                    20                      25                      30

Asn Ala Lys Ala Asn Arg  
                    35

## (2) INFORMATION FOR SEQ ID NO:212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /note= "motif E peptide from  
Saccharomyces cerevisiae  
ESTp (L8543.12)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ile Arg Ser Lys Ser Ser Lys Gly Ile Phe Arg  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```

Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn
1 5 10 15
Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val
 20 25 30
Glu Ile Glu Thr Leu Leu Met
 35

```

## (2) INFORMATION FOR SEQ ID NO:214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

Ile Cys His Gln Xaa Glu Tyr Tyr Phe Gly Asp Phe Asn Leu Pro Arg
1 5 10 15
Asp Lys Phe Leu Lys Glu Gln Ile Lys Leu Asp Glu Gly Trp Val Pro
 20 25 30
Leu Glu Ile Met Ile Lys
 35

```

## (2) INFORMATION FOR SEQ ID NO:215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

Ile Cys Glu Gln Ile Glu Tyr Tyr Phe Gly Asp His Asn Leu Pro Arg
1 5 10 15

```

Asp Lys Phe Leu Lys Gln Gln Ile Leu Leu Asp Asp Gly Trp Val Pro  
                   20                                  25                                  30

Leu Glu Thr Met Ile Lys  
                   35

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Ile Leu Arg Gln Val Glu Tyr Tyr Phe Gly Asp Ala Asn Leu Asn Arg  
   1                  5                                  10                                  15

Asp Lys Phe Leu Arg Glu Gln Ile Gly Lys Asn Glu Asp Gly Trp Val  
                   20                                  25                                  30

Pro Leu Ser Val Leu Val Thr  
                   35

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Cys Leu Lys Gln Val Glu Phe Tyr Phe Ser Glu Phe Asn Phe Pro Tyr  
   1                  5                                  10                                  15

Asp Arg Phe Leu Arg Thr Thr Ala Glu Lys Asn Asp Gly Trp Val Pro  
                   20                                  25                                  30

Ile Ser Thr Ile Ala Thr  
                   35

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2421 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 92..2251

(D) OTHER INFORMATION: /codon= (seq: "taa", aa: Gln)  
/codon= (seq: "tag", aa: Gln)  
/codon= (seq: "tga", aa: TRM)  
/product= "Tetrahymena thermophila  
80 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AACTCATTTA ATTACTAATT TAATCAACAA GATTGATAAA AAGCAGTAAA TAAAACCCAA | 60  |
| TAGATTTAAT TTAGAAAGTA TCAATTGAAA A ATG GAA ATT GAA AAC AAC TAA    | 112 |
| Met Glu Ile Glu Asn Asn Gln                                       |     |
| 1 5                                                               |     |
| GCA CAA TAG CCA AAA GCC GAA AAA TTG TGG TGG GAA CTT GAA TTA GAG   | 160 |
| Ala Gln Gln Pro Lys Ala Glu Lys Leu Trp Trp Glu Leu Glu Leu Glu   |     |
| 10 15 20                                                          |     |
| ATG CAA GAA AAC CAA AAT GAT ATA TAA GTT AGG GTT AAG ATT GAC GAT   | 208 |
| Met Gln Glu Asn Gln Asn Asp Ile Gln Val Arg Val Lys Ile Asp Asp   |     |
| 25 30 35                                                          |     |
| CCT AAG CAA TAT CTC GTG AAC GTC ACT GCA GCA TGT TTG TTG TAG GAA   | 256 |
| Pro Lys Gln Tyr Leu Val Asn Val Thr Ala Ala Cys Leu Leu Gln Glu   |     |
| 40 45 50 55                                                       |     |
| GGT AGT TAC TAC TAA GAT AAA GAT GAA AGA AGA TAT ATC ATC ACT AAA   | 304 |
| Gly Ser Tyr Tyr Gln Asp Lys Asp Glu Arg Arg Tyr Ile Ile Thr Lys   |     |
| 60 65 70                                                          |     |
| GCA CTT CTT GAG GTG GCT GAG TCT GAT CCT GAG TTC ATC TGC TAG TTG   | 352 |
| Ala Leu Leu Glu Val Ala Glu Ser Asp Pro Glu Phe Ile Cys Gln Leu   |     |
| 75 80 85                                                          |     |
| GCA GTC TAC ATC CGT AAT GAA CTT TAC ATC AGA ACT ACC ACT AAC TAC   | 400 |
| Ala Val Tyr Ile Arg Asn Glu Leu Tyr Ile Arg Thr Thr Thr Asn Tyr   |     |
| 90 95 100                                                         |     |
| ATT GTA GCA TTT TGT GTT GTC CAC AAG AAT ACT CAA CCA TTC ATC GAA   | 448 |
| Ile Val Ala Phe Cys Val Val His Lys Asn Thr Gln Pro Phe Ile Glu   |     |
| 105 110 115                                                       |     |
| AAG TAC TTC AAC AAA GCA GTA CTT TTG CCT AAT GAC TTA CTG GAA GTC   | 496 |
| Lys Tyr Phe Asn Lys Ala Val Leu Leu Pro Asn Asp Leu Leu Glu Val   |     |
| 120 125 130 135                                                   |     |
| TGT GAA TTT GCA TAG GTT CTC TAT ATT TTT GAT GCA ACT GAA TTC AAA   | 544 |
| Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp Ala Thr Glu Phe Lys   |     |
| 140 145 150                                                       |     |
| AAT TTG TAT CTT GAT AGG ATA CTT TCA TAA GAT ATT CGT AAG GAA CTC   | 592 |
| Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp Ile Arg Lys Glu Leu   |     |
| 155 160 165                                                       |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| ACT TTC CGT AAG TGT TTA CAA AGA TGC GTC AGA AGC AAG TTT TCT GAA<br>Thr Phe Arg Lys Cys Leu Gln Arg Cys Val Arg Ser Lys Phe Ser Glu<br>170 175 180     | 640  |
| TTC AAC GAA TAC TAA CTT GGT AAG TAT TGC ACT GAA TCC TAA CGT AAG<br>Phe Asn Glu Tyr Gln Leu Gly Lys Tyr Cys Thr Glu Ser Gln Arg Lys<br>185 190 195     | 688  |
| AAA ACA ATG TTC CGT TAC CTC TCA GTT ACC AAC AAG TAA AAG TGG GAT<br>Lys Thr Met Phe Arg Tyr Leu Ser Val Thr Asn Lys Gln Lys Trp Asp<br>200 205 210 215 | 736  |
| TAA ACT AAG AAG AAG AGA AAA GAG AAT CTC TTA ACC AAA CTT TAG GCA<br>Gln Thr Lys Lys Lys Arg Lys Glu Asn Leu Leu Thr Lys Leu Gln Ala<br>220 225 230     | 784  |
| ATA AAG GAA TCT GAA GAT AAG TCC AAG AGA GAA ACT GGA GAC ATA ATG<br>Ile Lys Glu Ser Glu Asp Lys Ser Lys Arg Glu Thr Gly Asp Ile Met<br>235 240 245     | 832  |
| AAC GTT GAA GAT GCA ATC AAG GCT TTA AAA CCA GCA GTT ATG AAG AAA<br>Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro Ala Val Met Lys Lys<br>250 255 260     | 880  |
| ATA GCC AAG AGA TAG AAT GCC ATG AAG AAA CAC ATG AAG GCA CCT AAA<br>Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His Met Lys Ala Pro Lys<br>265 270 275     | 928  |
| ATT CCT AAC TCT ACC TTG GAA TCA AAG TAC TTG ACC TTC AAG GAT CTC<br>Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu Thr Phe Lys Asp Leu<br>280 285 290 295 | 976  |
| ATT AAG TTC TGC CAT ATT TCT GAG CCT AAA GAA AGA GTC TAT AAG ATC<br>Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu Arg Val Tyr Lys Ile<br>300 305 310     | 1024 |
| CTT GGT AAA AAA TAC CCT AAG ACC GAA GAG GAA TAC AAA GCA GCC TTT<br>Leu Gly Lys Lys Tyr Pro Lys Thr Glu Glu Glu Tyr Lys Ala Ala Phe<br>315 320 325     | 1072 |
| GGT GAT TCT GCA TCT GCA CCC TTC AAT CCT GAA TTG GCT GGA AAG CGT<br>Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu Leu Ala Gly Lys Arg<br>330 335 340     | 1120 |
| ATG AAG ATT GAA ATC TCT AAA ACA TGG GAA AAT GAA CTC AGT GCA AAA<br>Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn Glu Leu Ser Ala Lys<br>345 350 355     | 1168 |
| GGC AAC ACT GCT GAG GTT TGG GAT AAT TTA ATT TCA AGC AAT TAA CTC<br>Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile Ser Ser Asn Gln Leu<br>360 365 370 375 | 1216 |
| CCA TAT ATG GCC ATG TTA CGT AAC TTG TCT AAC ATC TTA AAA GCC GGT<br>Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn Ile Leu Lys Ala Gly<br>380 385 390     | 1264 |
| GTT TCA GAT ACT ACA CAC TCT ATT GTG ATC AAC AAG ATT TGT GAG CCC<br>Val Ser Asp Thr Thr His Ser Ile Val Ile Asn Lys Ile Cys Glu Pro<br>395 400 405     | 1312 |

|                                                                 |      |
|-----------------------------------------------------------------|------|
| AAG GCC GTT GAG AAC TCC AAG ATG TTC CCT CTT CAA TTC TTT AGT GCC | 1360 |
| Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu Gln Phe Phe Ser Ala |      |
| 410 415 420                                                     |      |
| ATT GAA GCT GTT AAT GAA GCA GTT ACT AAG GGA TTC AAG GCC AAG AAG | 1408 |
| Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly Phe Lys Ala Lys Lys |      |
| 425 430 435                                                     |      |
| AGA GAA AAT ATG AAT CTT AAA GGT CAA ATC GAA GCA GTA AAG GAA GTT | 1456 |
| Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu Ala Val Lys Glu Val |      |
| 440 445 450 455                                                 |      |
| GTT GAA AAA ACC GAT GAA GAG AAG AAA GAT ATG GAG TTG GAG TAA ACC | 1504 |
| Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met Glu Leu Glu Gln Thr |      |
| 460 465 470                                                     |      |
| GAA GAA GGA GAA TTT GTT AAA GTC AAC GAA GGA ATT GGC AAG CAA TAC | 1552 |
| Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly Ile Gly Lys Gln Tyr |      |
| 475 480 485                                                     |      |
| ATT AAC TCC ATT GAA CTT GCA ATC AAG ATA GCA GTT AAC AAG AAT TTA | 1600 |
| Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu |      |
| 490 495 500                                                     |      |
| GAT GAA ATC AAA GGA CAC ACT GCA ATC TTC TCT GAT GTT TCT GGT TCT | 1648 |
| Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser |      |
| 505 510 515                                                     |      |
| ATG AGT ACC TCA ATG TCA GGT GGA GCC AAG AAG TAT GGT TCC GTT CGT | 1696 |
| Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg |      |
| 520 525 530 535                                                 |      |
| ACT TGT CTC GAG TGT GCA TTA GTC CTT GGT TTG ATG GTA AAA TAA CGT | 1744 |
| Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg |      |
| 540 545 550                                                     |      |
| TGT GAA AAG TCC TCA TTC TAC ATC TTC AGT TCA CCT AGT TCT CAA TGC | 1792 |
| Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys |      |
| 555 560 565                                                     |      |
| AAT AAG TGT TAC TTA GAA GTT GAT CTC CCT GGA GAC GAA CTC CGT CCT | 1840 |
| Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro |      |
| 570 575 580                                                     |      |
| TCT ATG TAA AAA CTT TTG CAA GAG AAA GGA AAA CTT GGT GGT GGT ACT | 1888 |
| Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys Leu Gly Gly Gly Thr |      |
| 585 590 595                                                     |      |
| GAT TTC CCC TAT GAG TGC ATT GAT GAA TGG ACA AAG AAT AAA ACT CAC | 1936 |
| Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr Lys Asn Lys Thr His |      |
| 600 605 610 615                                                 |      |
| GTA GAC AAT ATC GTT ATT TTG TCT GAT ATG ATG ATT GCA GAA GGA TAT | 1984 |
| Val Asp Asn Ile Val Ile Leu Ser Asp Met Met Ile Ala Glu Gly Tyr |      |
| 620 625 630                                                     |      |
| TCA GAT ATC AAT GTT AGA GGC AGT TCC ATT GTT AAC AGC ATC AAA AAG | 2032 |
| Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val Asn Ser Ile Lys Lys |      |
| 635 640 645                                                     |      |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| TAC AAG GAT GAA GTA AAT CCT AAC ATT AAA ATC TTT GCA GTT GAC TTA   | 2080 |
| Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile Phe Ala Val Asp Leu   |      |
| 650 655 660                                                       |      |
| GAA GGT TAC GGA AAG TGC CTT AAT CTA GGT GAT GAG TTC AAT GAA AAC   | 2128 |
| Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp Glu Phe Asn Glu Asn   |      |
| 665 670 675                                                       |      |
| AAC TAC ATC AAG ATA TTC GGT ATG AGC GAT TCA ATC TTA AAG TTC ATT   | 2176 |
| Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser Ile Leu Lys Phe Ile   |      |
| 680 685 690 695                                                   |      |
| TCA GCC AAG CAA GGA GGA GCA AAT ATG GTC GAA GTT ATC AAA AAC TTT   | 2224 |
| Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu Val Ile Lys Asn Phe   |      |
| 700 705 710                                                       |      |
| GCC CTT CAA AAA ATA GGA CAA AAG TGAGTTTCTT GAGATTCTTC TATAACAAAA  | 2278 |
| Ala Leu Gln Lys Ile Gly Gln Lys                                   |      |
| 715                                                               |      |
| ATCTCACCCC ACTTTTTTGT TTTATTGCAT AGCCATTATG AAATTTAAAT TATTATCTAT | 2338 |
| TTATTTAAGT TACTTACATA GTTTATGTAT CGCAGTCTAT TAGCCTATTC AAATGATTCT | 2398 |
| GCAAAGAACA AAAAAGATTA AAA                                         | 2421 |

## (2) INFORMATION FOR SEQ ID NO:219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ile | Glu | Asn | Asn | Gln | Ala | Gln | Gln | Pro | Lys | Ala | Glu | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Trp | Glu | Leu | Glu | Leu | Glu | Met | Gln | Glu | Asn | Gln | Asn | Asp | Ile | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Arg | Val | Lys | Ile | Asp | Asp | Pro | Lys | Gln | Tyr | Leu | Val | Asn | Val | Thr |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ala | Cys | Leu | Leu | Gln | Glu | Gly | Ser | Tyr | Tyr | Gln | Asp | Lys | Asp | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Tyr | Ile | Ile | Thr | Lys | Ala | Leu | Leu | Glu | Val | Ala | Glu | Ser | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Glu | Phe | Ile | Cys | Gln | Leu | Ala | Val | Tyr | Ile | Arg | Asn | Glu | Leu | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Arg | Thr | Thr | Thr | Asn | Tyr | Ile | Val | Ala | Phe | Cys | Val | Val | His | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Thr | Gln | Pro | Phe | Ile | Glu | Lys | Tyr | Phe | Asn | Lys | Ala | Val | Leu | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |



Pro Asn Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile  
 130 135 140

Phe Asp Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser  
 145 150 155 160

Gln Asp Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys  
 165 170 175

Val Arg Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr  
 180 185 190

Cys Thr Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val  
 195 200 205

Thr Asn Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn  
 210 215 220

Leu Leu Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys  
 225 230 235 240

Arg Glu Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu  
 245 250 255

Lys Pro Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys  
 260 265 270

Lys His Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys  
 275 280 285

Tyr Leu Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro  
 290 295 300

Lys Glu Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu  
 305 310 315 320

Glu Glu Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn  
 325 330 335

Pro Glu Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp  
 340 345 350

Glu Asn Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn  
 355 360 365

Leu Ile Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu  
 370 375 380

Ser Asn Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val  
 385 390 395 400

Ile Asn Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe  
 405 410 415

Pro Leu Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr  
 420 425 430

Lys Gly Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln  
 435 440 445

Ile Glu Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys  
 450 455 460  
 Asp Met Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn  
 465 470 475 480  
 Glu Gly Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys  
 485 490 495  
 Ile Ala Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile  
 500 505 510  
 Phe Ser Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala  
 515 520 525  
 Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu  
 530 535 540  
 Gly Leu Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe  
 545 550 555 560  
 Ser Ser Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu  
 565 570 575  
 Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys  
 580 585 590  
 Gly Lys Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu  
 595 600 605  
 Trp Thr Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp  
 610 615 620  
 Met Met Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser  
 625 630 635 640  
 Ile Val Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile  
 645 650 655  
 Lys Ile Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu  
 660 665 670  
 Gly Asp Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser  
 675 680 685  
 Asp Ser Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met  
 690 695 700  
 Val Glu Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly Gln Lys  
 705 710 715

## (2) INFORMATION FOR SEQ ID NO:220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2829 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 47..2665  
 (D) OTHER INFORMATION: /codon= (seq: "taa", aa: Gln)  
 /codon= (seq: "tag", aa: Gln)  
 /codon= (seq: "tga", aa: TRM)  
 /product= "Tetrahymena thermophila  
 95 kDa protein subunit"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

TCAATACTAT TAATTAATAA ATAAAAAAA GCAAACTACA AAGAAA ATG TCA AGG 55  
 Met Ser Arg  
 1

CGT AAC TAA AAA AAG CCA TAG GCT CCT ATA GGC AAT GAA ACA AAT CTT 103  
 Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu Thr Asn Leu  
 5 10 15

GAT TTT GTA TTA CAA AAT CTA GAA GTT TAC AAA AGC CAG ATT GAG CAT 151  
 Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln Ile Glu His  
 20 25 30 35

TAT AAG ACC TAG TAG TAA TAG ATC AAA GAG GAG GAT CTC AAG CTT TTA 199  
 Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu Lys Leu Leu  
 40 45 50

AAG TTC AAA AAT TAA GAT TAG GAT GGA AAC TCT GGC AAC GAT GAT GAT 247  
 Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn Asp Asp Asp  
 55 60 65

GAT GAA GAA AAC AAC TCA AAT AAA TAA TAA GAA TTA TTA AGG AGA GTC 295  
 Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu Arg Arg Val  
 70 75 80

AAT TAG ATT AAG TAG CAA GTT TAA TTG ATA AAA AAA GTT GGT TCT AAG 343  
 Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val Gly Ser Lys  
 85 90 95

GTA GAG AAA GAT TTG AAT TTG AAC GAA GAT GAA AAC AAA AAG AAT GGA 391  
 Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys Lys Asn Gly  
 100 105 110 115

CTT TCT GAA TAG CAA GTG AAA GAA GAG TAA TTA AGA ACG ATT ACT GAA 439  
 Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr Ile Thr Glu  
 120 125 130

GAA TAG GTT AAG TAT TAA AAT TTA GTA TTT AAC ATG GAC TAC CAG TTA 487  
 Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp Tyr Gln Leu  
 135 140 145

GAT TTA AAT GAG AGT GGT GGC CAT AGA AGA CAC AGA AGA GAA ACA GAT 535  
 Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg Glu Thr Asp  
 150 155 160

TAT GAT ACT GAA AAA TGG TTT GAA ATA TCT CAT GAC CAA AAA AAT TAT 583  
 Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln Lys Asn Tyr  
 165 170 175

|                                                                 |      |
|-----------------------------------------------------------------|------|
| GTA TCA ATT TAC GCC AAC TAA AAG ACA TCA TAT TGT TGG TGG CTT AAA | 631  |
| Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp Trp Leu Lys |      |
| 180 185 190 195                                                 |      |
| GAT TAT TTT AAT AAA AAC AAT TAT GAT CAT CTT AAT GTA AGC ATT AAC | 679  |
| Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val Ser Ile Asn |      |
| 200 205 210                                                     |      |
| AGA CTA GAA ACT GAA GCC GAA TTC TAT GCC TTT GAT GAT TTT TCA CAA | 727  |
| Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp Phe Ser Gln |      |
| 215 220 225                                                     |      |
| ACA ATC AAA CTT ACT AAT AAT TCT TAC TAG ACT GTT AAC ATA GAC GTT | 775  |
| Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn Ile Asp Val |      |
| 230 235 240                                                     |      |
| AAT TTT GAT AAT AAT CTC TGT ATA CTC GCA TTG CTT AGA TTT TTA TTA | 823  |
| Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg Phe Leu Leu |      |
| 245 250 255                                                     |      |
| TCA CTA GAA AGA TTC AAT ATT TTG AAT ATA AGA TCT TCT TAT ACA AGA | 871  |
| Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser Tyr Thr Arg |      |
| 260 265 270 275                                                 |      |
| AAT TAA TAT AAT TTT GAG AAA ATT GGT GAG CTA CTT GAA ACT ATC TTC | 919  |
| Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu Thr Ile Phe |      |
| 280 285 290                                                     |      |
| GCA GTT GTC TTT TCT CAT CGC CAC TTA CAA GGC ATT CAT TTA CAA GTT | 967  |
| Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His Leu Gln Val |      |
| 295 300 305                                                     |      |
| CCT TGC GAA GCG TTC TAA TAT TTA GTT AAC TCC TCA TCA TAA ATT AGC | 1015 |
| Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser Gln Ile Ser |      |
| 310 315 320                                                     |      |
| GTT AAA GAT AGC TAA TTA TAG GTA TAC TCT TTC TCT ACA GAC TTA AAA | 1063 |
| Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr Asp Leu Lys |      |
| 325 330 335                                                     |      |
| TTA GTT GAC ACT AAC AAA GTC CAA GAT TAT TTT AAG TTC TTA TAA GAA | 1111 |
| Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe Leu Gln Glu |      |
| 340 345 350 355                                                 |      |
| TTC CCT CGT TTG ACT CAT GTA AGC TAG TAG GCT ATC CCA GTT AGT GCT | 1159 |
| Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro Val Ser Ala |      |
| 360 365 370                                                     |      |
| ACT AAC GCT GTA GAG AAC CTC AAT GTT TTA CTT AAA AAG GTC AAG CAT | 1207 |
| Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys Val Lys His |      |
| 375 380 385                                                     |      |
| GCT AAT CTT AAT TTA GTT TCT ATC CCT ACC TAA TTC AAT TTT GAT TTC | 1255 |
| Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn Phe Asp Phe |      |
| 390 395 400                                                     |      |
| TAC TTT GTT AAT TTA TAA CAT TTG AAA TTA GAG TTT GGA TTA GAA CCA | 1303 |
| Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly Leu Glu Pro |      |
| 405 410 415                                                     |      |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAT ATT TTG ACA AAA CAA AAG CTT GAA AAT CTA CTT TTG AGT ATA AAA<br>Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Ser Ile Lys<br>420 425 430 435     | 1351 |
| TAA TCA AAA AAT CTT AAA TTT TTA AGA TTA AAC TTT TAC ACC TAC GTT<br>Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr Thr Tyr Val<br>440 445 450     | 1399 |
| GCT TAA GAA ACC TCC AGA AAA CAG ATA TTA AAA CAA GCT ACA ACA ATC<br>Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala Thr Thr Ile<br>455 460 465     | 1447 |
| AAA AAT CTC AAA AAC AAT AAA AAT CAA GAA GAA ACT CCT GAA ACT AAA<br>Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro Glu Thr Lys<br>470 475 480     | 1495 |
| GAT GAA ACT CCA AGC GAA AGC ACA AGT GGT ATG AAA TTT TTT GAT CAT<br>Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe Phe Asp His<br>485 490 495     | 1543 |
| CTT TCT GAA TTA ACC GAG CTT GAA GAT TTC AGC GTT AAC TTG TAA GCT<br>Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn Leu Gln Ala<br>500 505 510 515 | 1591 |
| ACC CAA GAA ATT TAT GAT AGC TTG CAC AAA CTT TTG ATT AGA TCA ACA<br>Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile Arg Ser Thr<br>520 525 530     | 1639 |
| AAT TTA AAG AAG TTC AAA TTA AGT TAC AAA TAT GAA ATG GAA AAG AGT<br>Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met Glu Lys Ser<br>535 540 545     | 1687 |
| AAA ATG GAT ACA TTC ATA GAT CTT AAG AAT ATT TAT GAA ACC TTA AAC<br>Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu Thr Leu Asn<br>550 555 560     | 1735 |
| AAT CTT AAA AGA TGC TCT GTT AAT ATA TCA AAT CCT CAT GGA AAC ATT<br>Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His Gly Asn Ile<br>565 570 575     | 1783 |
| TCT TAT GAA CTG ACA AAT AAA GAT TCT ACT TTT TAT AAA TTT AAG CTG<br>Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys Phe Lys Leu<br>580 585 590 595 | 1831 |
| ACC TTA AAC TAA GAA TTA TAA CAC GCT AAG TAT ACT TTT AAG TAG AAC<br>Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe Lys Gln Asn<br>600 605 610     | 1879 |
| GAA TTT TAA TTT AAT AAC GTT AAA AGT GCA AAA ATT GAA TCT TCC TCA<br>Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser<br>615 620 625     | 1927 |
| TTA GAA AGC TTA GAA GAT ATT GAT AGT CTT TGC AAA TCT ATT GCT TCT<br>Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser<br>630 635 640     | 1975 |
| TGT AAA AAT TTA CAA AAT GTT AAT ATT ATC GCC AGT TTG CTC TAT CCC<br>Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro<br>645 650 655     | 2023 |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAC AAT ATT TAG AAA AAT CCT TTC AAT AAG CCC AAT CTT CTA TTT TTC<br>Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe<br>660 665 670 675 | 2071 |
| AAG CAA TTT GAA TAA TTG AAA AAT TTG GAA AAT GTA TCT ATC AAC TGT<br>Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys<br>680 685 690     | 2119 |
| ATT CTT GAT CAG CAT ATA CTT AAT TCT ATT TCA GAA TTC TTA GAA AAG<br>Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys<br>695 700 705     | 2167 |
| AAT AAA AAA ATA AAA GCA TTC ATT TTG AAA AGA TAT TAT TTA TTA CAA<br>Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr Leu Leu Gln<br>710 715 720     | 2215 |
| TAT TAT CTT GAT TAT ACT AAA TTA TTT AAA ACA CTT CAA TAG TTA CCT<br>Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln Gln Leu Pro<br>725 730 735     | 2263 |
| GAA TTA AAT TAA GTT TAC ATT AAT TAG CAA TTA GAA GAA TTG ACT GTG<br>Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu Leu Thr Val<br>740 745 750 755 | 2311 |
| AGT GAA GTA CAT AAG TAA GTA TGG GAA AAC CAC AAG CAA AAA GCT TTC<br>Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln Lys Ala Phe<br>760 765 770     | 2359 |
| TAT GAA CCA TTA TGT GAG TTT ATC AAA GAA TCA TCC TAA ACC CTT TAG<br>Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln Thr Leu Gln<br>775 780 785     | 2407 |
| CTA ATA GAT TTT GAC CAA AAC ACT GTA AGT GAT GAC TCT ATT AAA AAG<br>Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser Ile Lys Lys<br>790 795 800     | 2455 |
| ATT TTA GAA TCT ATA TCT GAG TCT AAG TAT CAT CAT TAT TTG AGA TTG<br>Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr Leu Arg Leu<br>805 810 815     | 2503 |
| AAC CCT AGT TAA TCT AGC AGT TTA ATT AAA TCT GAA AAC GAA GAA ATT<br>Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn Glu Glu Ile<br>820 825 830 835 | 2551 |
| TAA GAA CTT CTC AAA GCT TGC GAC GAA AAA GGT GTT TTA GTA AAA GCA<br>Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu Val Lys Ala<br>840 845 850     | 2599 |
| TAC TAT AAA TTC CCT CTA TGT TTA CCA ACT GGT ACT TAT TAC GAT TAC<br>Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr Tyr Asp Tyr<br>855 860 865     | 2647 |
| AAT TCA GAT AGA TGG TGATTAATTA AATATTAGTT TAAATAAATA TTAAATATTG<br>Asn Ser Asp Arg Trp<br>870                                                         | 2702 |
| AATATTTCTT TGCTTATTAT TTGAATAATA CATACAATAG TCATTTTATG TGTTTTGAAT                                                                                     | 2762 |
| ATATTTTAGT TATTTAATTC ATTATTTTAA GTAAATAATT ATTTTTCAT CATTTTTAA                                                                                       | 2822 |
| AAAATCG                                                                                                                                               | 2829 |

## (2) INFORMATION FOR SEQ ID NO:221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu
 1 5 10 15

Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln
 20 25 30

Ile Glu His Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu
 35 40 45

Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn
 50 55 60

Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu
 65 70 75 80

Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val
 85 90 95

Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys
 100 105 110

Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr
 115 120 125

Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp
 130 135 140

Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg
 145 150 155 160

Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln
 165 170 175

Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp
 180 185 190

Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val
 195 200 205

Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp
 210 215 220

Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn
 225 230 235 240

Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg
 245 250 255

Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser
 260 265 270

```

Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu  
 275 280 285  
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His  
 290 295 300  
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser  
 305 310 315 320  
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr  
 325 330 335  
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe  
 340 345 350  
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro  
 355 360 365  
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys  
 370 375 380  
 Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn  
 385 390 395 400  
 Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly  
 405 410 415  
 Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu  
 420 425 430  
 Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr  
 435 440 445  
 Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala  
 450 455 460  
 Thr Thr Ile Lys Asn Leu Lys Asn Asn Lys Asn Gln Glu Glu Thr Pro  
 465 470 475 480  
 Glu Thr Lys Asp Glu Thr Pro Ser Glu Ser Thr Ser Gly Met Lys Phe  
 485 490 495  
 Phe Asp His Leu Ser Glu Leu Thr Glu Leu Glu Asp Phe Ser Val Asn  
 500 505 510  
 Leu Gln Ala Thr Gln Glu Ile Tyr Asp Ser Leu His Lys Leu Leu Ile  
 515 520 525  
 Arg Ser Thr Asn Leu Lys Lys Phe Lys Leu Ser Tyr Lys Tyr Glu Met  
 530 535 540  
 Glu Lys Ser Lys Met Asp Thr Phe Ile Asp Leu Lys Asn Ile Tyr Glu  
 545 550 555 560  
 Thr Leu Asn Asn Leu Lys Arg Cys Ser Val Asn Ile Ser Asn Pro His  
 565 570 575  
 Gly Asn Ile Ser Tyr Glu Leu Thr Asn Lys Asp Ser Thr Phe Tyr Lys  
 580 585 590



Phe Lys Leu Thr Leu Asn Gln Glu Leu Gln His Ala Lys Tyr Thr Phe  
 595 600 605  
 Lys Gln Asn Glu Phe Gln Phe Asn Asn Val Lys Ser Ala Lys Ile Glu  
 610 615 620  
 Ser Ser Ser Leu Glu Ser Leu Glu Asp Ile Asp Ser Leu Cys Lys Ser  
 625 630 635 640  
 Ile Ala Ser Cys Lys Asn Leu Gln Asn Val Asn Ile Ile Ala Ser Leu  
 645 650 655  
 Leu Tyr Pro Asn Asn Ile Gln Lys Asn Pro Phe Asn Lys Pro Asn Leu  
 660 665 670  
 Leu Phe Phe Lys Gln Phe Glu Gln Leu Lys Asn Leu Glu Asn Val Ser  
 675 680 685  
 Ile Asn Cys Ile Leu Asp Gln His Ile Leu Asn Ser Ile Ser Glu Phe  
 690 695 700  
 Leu Glu Lys Asn Lys Lys Ile Lys Ala Phe Ile Leu Lys Arg Tyr Tyr  
 705 710 715 720  
 Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln  
 725 730 735  
 Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu  
 740 745 750  
 Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln  
 755 760 765  
 Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln  
 770 775 780  
 Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser  
 785 790 795 800  
 Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr  
 805 810 815  
 Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn  
 820 825 830  
 Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu  
 835 840 845  
 Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr  
 850 855 860  
 Tyr Asp Tyr Asn Ser Asp Arg Trp  
 865 870

## (2) INFORMATION FOR SEQ ID NO:222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..884
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae  
ESTp (L8543.12) "

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu
1 5 10 15
Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn
20 25 30
Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg
35 40 45
Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val
50 55 60
Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn
65 70 75 80
Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn
85 90 95
Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly
100 105 110
Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val
115 120 125
Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe
130 135 140
Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys
145 150 155 160
Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys
165 170 175
Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn
180 185 190
Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser
195 200 205
Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr
210 215 220

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Val | Lys | Ile | Pro | Gln | Arg | Leu | Lys | Val | Arg | Ile | Asn | Leu | Thr | 225 | 230 | 235 | 240 |
| Leu | Gln | Lys | Leu | Leu | Lys | Arg | His | Lys | Arg | Leu | Asn | Tyr | Val | Ser | Ile | 245 | 250 | 255 |     |
| Leu | Asn | Ser | Ile | Cys | Pro | Pro | Leu | Glu | Gly | Thr | Val | Leu | Asp | Leu | Ser | 260 | 265 | 270 |     |
| His | Leu | Ser | Arg | Gln | Ser | Pro | Lys | Glu | Arg | Val | Leu | Lys | Phe | Ile | Ile | 275 | 280 | 285 |     |
| Val | Ile | Leu | Gln | Lys | Leu | Leu | Pro | Gln | Glu | Met | Phe | Gly | Ser | Lys | Lys | 290 | 295 | 300 |     |
| Asn | Lys | Gly | Lys | Ile | Ile | Lys | Asn | Leu | Asn | Leu | Leu | Leu | Ser | Leu | Pro | 305 | 310 | 315 | 320 |
| Leu | Asn | Gly | Tyr | Leu | Pro | Phe | Asp | Ser | Leu | Leu | Lys | Lys | Leu | Arg | Leu | 325 | 330 | 335 |     |
| Lys | Asp | Phe | Arg | Trp | Leu | Phe | Ile | Ser | Asp | Ile | Trp | Phe | Thr | Lys | His | 340 | 345 | 350 |     |
| Asn | Phe | Glu | Asn | Leu | Asn | Gln | Leu | Ala | Ile | Cys | Phe | Ile | Ser | Trp | Leu | 355 | 360 | 365 |     |
| Phe | Arg | Gln | Leu | Ile | Pro | Lys | Ile | Ile | Gln | Thr | Phe | Phe | Tyr | Cys | Thr | 370 | 375 | 380 |     |
| Glu | Ile | Ser | Ser | Thr | Val | Thr | Ile | Val | Tyr | Phe | Arg | His | Asp | Thr | Trp | 385 | 390 | 395 | 400 |
| Asn | Lys | Leu | Ile | Thr | Pro | Phe | Ile | Val | Glu | Tyr | Phe | Lys | Thr | Tyr | Leu | 405 | 410 | 415 |     |
| Val | Glu | Asn | Asn | Val | Cys | Arg | Asn | His | Asn | Ser | Tyr | Thr | Leu | Ser | Asn | 420 | 425 | 430 |     |
| Phe | Asn | His | Ser | Lys | Met | Arg | Ile | Ile | Pro | Lys | Lys | Ser | Asn | Asn | Glu | 435 | 440 | 445 |     |
| Phe | Arg | Ile | Ile | Ala | Ile | Pro | Cys | Arg | Gly | Ala | Asp | Glu | Glu | Glu | Phe | 450 | 455 | 460 |     |
| Thr | Ile | Tyr | Lys | Glu | Asn | His | Lys | Asn | Ala | Ile | Gln | Pro | Thr | Gln | Lys | 465 | 470 | 475 | 480 |
| Ile | Leu | Glu | Tyr | Leu | Arg | Asn | Lys | Arg | Pro | Thr | Ser | Phe | Thr | Lys | Ile | 485 | 490 | 495 |     |
| Tyr | Ser | Pro | Thr | Gln | Ile | Ala | Asp | Arg | Ile | Lys | Glu | Phe | Lys | Gln | Arg | 500 | 505 | 510 |     |
| Leu | Leu | Lys | Lys | Phe | Asn | Asn | Val | Leu | Pro | Glu | Leu | Tyr | Phe | Met | Lys | 515 | 520 | 525 |     |
| Phe | Asp | Val | Lys | Ser | Cys | Tyr | Asp | Ser | Ile | Pro | Arg | Met | Glu | Cys | Met | 530 | 535 | 540 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Leu | Lys | Asp | Ala | Leu | Lys | Asn | Glu | Asn | Gly | Phe | Phe | Val | Arg | 545 | 550 | 555 | 560 |
| Ser | Gln | Tyr | Phe | Phe | Asn | Thr | Asn | Thr | Gly | Val | Leu | Lys | Leu | Phe | Asn | 565 | 570 | 575 |     |
| Val | Val | Asn | Ala | Ser | Arg | Val | Pro | Lys | Pro | Tyr | Glu | Leu | Tyr | Ile | Asp | 580 | 585 | 590 |     |
| Asn | Val | Arg | Thr | Val | His | Leu | Ser | Asn | Gln | Asp | Val | Ile | Asn | Val | Val | 595 | 600 | 605 |     |
| Glu | Met | Glu | Ile | Phe | Lys | Thr | Ala | Leu | Trp | Val | Glu | Asp | Lys | Cys | Tyr | 610 | 615 | 620 |     |
| Ile | Arg | Glu | Asp | Gly | Leu | Phe | Gln | Gly | Ser | Ser | Leu | Ser | Ala | Pro | Ile | 625 | 630 | 635 | 640 |
| Val | Asp | Leu | Val | Tyr | Asp | Asp | Leu | Leu | Glu | Phe | Tyr | Ser | Glu | Phe | Lys | 645 | 650 | 655 |     |
| Ala | Ser | Pro | Ser | Gln | Asp | Thr | Leu | Ile | Leu | Lys | Leu | Ala | Asp | Asp | Phe | 660 | 665 | 670 |     |
| Leu | Ile | Ile | Ser | Thr | Asp | Gln | Gln | Gln | Val | Ile | Asn | Ile | Lys | Lys | Leu | 675 | 680 | 685 |     |
| Ala | Met | Gly | Gly | Phe | Gln | Lys | Tyr | Asn | Ala | Lys | Ala | Asn | Arg | Asp | Lys | 690 | 695 | 700 |     |
| Ile | Leu | Ala | Val | Ser | Ser | Gln | Ser | Asp | Asp | Asp | Thr | Val | Ile | Gln | Phe | 705 | 710 | 715 | 720 |
| Cys | Ala | Met | His | Ile | Phe | Val | Lys | Glu | Leu | Glu | Val | Trp | Lys | His | Ser | 725 | 730 | 735 |     |
| Ser | Thr | Met | Asn | Asn | Phe | His | Ile | Arg | Ser | Lys | Ser | Ser | Lys | Gly | Ile | 740 | 745 | 750 |     |
| Phe | Arg | Ser | Leu | Ile | Ala | Leu | Phe | Asn | Thr | Arg | Ile | Ser | Tyr | Lys | Thr | 755 | 760 | 765 |     |
| Ile | Asp | Thr | Asn | Leu | Asn | Ser | Thr | Asn | Thr | Val | Leu | Met | Gln | Ile | Asp | 770 | 775 | 780 |     |
| His | Val | Val | Lys | Asn | Ile | Ser | Glu | Cys | Tyr | Lys | Ser | Ala | Phe | Lys | Asp | 785 | 790 | 795 | 800 |
| Leu | Ser | Ile | Asn | Val | Thr | Gln | Asn | Met | Gln | Phe | His | Ser | Phe | Leu | Gln | 805 | 810 | 815 |     |
| Arg | Ile | Ile | Glu | Met | Thr | Val | Ser | Gly | Cys | Pro | Ile | Thr | Lys | Cys | Asp | 820 | 825 | 830 |     |
| Pro | Leu | Ile | Glu | Tyr | Glu | Val | Arg | Phe | Thr | Ile | Leu | Asn | Gly | Phe | Leu | 835 | 840 | 845 |     |
| Glu | Ser | Leu | Ser | Ser | Asn | Thr | Ser | Lys | Phe | Lys | Asp | Asn | Ile | Ile | Leu | 850 | 855 | 860 |     |

Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile  
 865 870 875 880

His Ile Val Asn

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Leu Cys Val Ser Tyr Ile Leu Ser Ser Phe Tyr Tyr Ala Asn Leu Glu  
 1 5 10 15  
 Glu Asn Ala Leu Gln Phe Leu Arg Lys Glu Ser Met Asp Pro Glu Lys  
 20 25 30  
 Pro Glu Thr Asn Leu Leu Met Arg Leu Thr  
 35 40

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu  
 1 5 10 15  
 Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn  
 20 25 30  
 Pro Asn Val Asn Leu Leu Met Arg Leu Thr  
 35 40

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2631 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2631

(D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| ATTTATACTC ATGAAAATCT TATTCGAGTT CATTCAAGAC AAGCTTGACA TTGATCTACA  | 60   |
| GACCAACAGT ACTTACAAAG AAAATTTAAA ATGTGGTCAC TTCAATGGCC TCGATGAAAT  | 120  |
| TCTAACTACG TGTTTCGCAC TACCAAATTC AAGAAAAATA GCATTACCAT GCCTTCCTGG  | 180  |
| TGACTTAAGC CACAAAGCAG TCATTGATCA CTGCATCATT TACCTGTTGA CGGGCGAATT  | 240  |
| ATACAACAAC GTACTAACAT TTGGCTATAA AATAGCTAGA AATGAAGATG TCAACAATAG  | 300  |
| TCTTTTTTGC CATTCTGCAA ATGTTAACGT TACGTTACTG AAAGGCGCTG CTTGGAAAAT  | 360  |
| GTTCCACAGT TTGGTCGGTA CATACGCATT CGTTGATTTA TTGATCAATT ATACAGTAAT  | 420  |
| TCAATTTAAT GGGCAGTTTT TCACTCAAAT CGTGGGTAAC AGATGTAACG AACCTCATCT  | 480  |
| GCGGCCCCAA TGGGTCCAAC GATCATCCTC ATCATGCGCA ACTGCTGCGC AAATCAAACA  | 540  |
| ACTTACAGAA CCAGTGACAA ATAAACAATT CTTACACAAG CTCAATATAA ATTCTCTTTC  | 600  |
| TTTTTTTCCT TATAGCAAGA TCCTTCCTTC ATCATCATCT ATCAAAAAGC TAACTGACTT  | 660  |
| CAGAGAAGCT ATTTTTCCTA CAAATTGCTT TAAAATTCCT CAGAGACTAA AGGTACGAAT  | 720  |
| TAATTTGACG CTGCAAAAGC TATTAAAGAG ACATAAGCGT TTGAATTACG TTTCTATTTT  | 780  |
| TAATAGTATT TGCCCAACAT TGGAAAGGAC CGTATTGGAC TTGTCCGATT TGAGTAGGCA  | 840  |
| ATACCCAAAG GAACGAGTCT TGAAATTTAT CATTGTTATT TTACAGAAGT TATTACCCCA  | 900  |
| AGAAATGTTT GGCTCAAGA AAAATATAGG AAAAATTATC AAGAATCTAA ATCTTTTATT   | 960  |
| AAGTTTACCC TTAAATGGCT ATTTACCATT TGATAGTTTG TTGAAAAAGT TAAGATTAAA  | 1020 |
| GGATTTTCGG TGSTTGTTCA TTTCTGATAT TTGGTTCACC AAGCACAATT TTGAAAACCT  | 1080 |
| GAATCAATTG GCGATTTGTT TCATTTCTCTG GCTATTTAGA CAACTAATTC CCAAAATTAT | 1140 |
| ACAGACTTTT TTTTACTGCA CCGAAATATC TTCTACAGTG ACAATTGTTT ACTTTAGACA  | 1200 |
| TGATACTTGG AATAAACTTA TCACCCCTTT TATCGTAGAA TATTTTAAGA CGTACTTAGT  | 1260 |
| CGAAAACAAC GTATGTAGAA ACCATAATAG TTACACGTTG TCCAATTTCA ATCATAGCAA  | 1320 |
| AATGAGGATT ATACCAAAA AAAGTAATTA TGAGTTCAGG ATTATTGCCA TCCCATGCAG   | 1380 |
| AGGGGCAGAC GAAGAAGAAT TCACAATTTA TAAGGAGAAT CACAAAAATG CTATCCAGCC  | 1440 |
| CACTCAAAAA ATTTTAGAAT ACCTAAGAAA CAAAAGGCCG ACTAGTTTTA CTAAAATATA  | 1500 |
| TTCTCCAACG CAAATAGCTG ACCGTATCAA AGAATTTAAG CAGAGACTTT TAAAGAAATT  | 1560 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TAATAATGTC TTACCAGAGC TTTATTTTCAT GAAATTTGAT GTCAAATCTT GCTATGATTC | 1620 |
| CATACCAAGG ATGGAATGTA TGAGGATACT CAAGGATGCG CTAAAAAATG AAAATGGGTT  | 1680 |
| TTTCGTTAGA TCTCAATATT TCTTCAATAC CAATACAGGT GTATTGAAGT TATTTAATGT  | 1740 |
| TGTTAACGCT AGCAGAGTAC CAAAACCTTA TGAGCTATAC ATAGATAATG TGAGGACGGT  | 1800 |
| TCATTTATCA AATCAGGATG TTATAAACGT TGTAGAGATG GAAATATTTA AAACAGCTTT  | 1860 |
| GTGGGTTGAA GATAAGTGCT ACATTAGAGA AGATGGTCTT TTTCAGGGCT CTAGTTTATC  | 1920 |
| TGCTCCGATC GTTGATTTGG TGTATGACGA TCTTCTGGAG TTTTATAGCG AGTTTAAAGC  | 1980 |
| CAGTCCTAGC CAGGACACAT TAATTTTAAA ACTGGCTGAC GATTTCTTA TAATATCAAC   | 2040 |
| AGACCAACAG CAAGTGATCA ATATCAAAAA GCTTGCCATG GCGGATTTT AAAAATATAA   | 2100 |
| TGCGAAAGCC AATAGAGACA AAATTTTAGC CGTAAGCTCC CAATCAGATG ATGATACGGT  | 2160 |
| TATTCAATTT TGTGCAATGC ACATATTTGT TAAAGAATTG GAAGTTTGGA AACATTCAAG  | 2220 |
| CACAATGAAT AATTTCATA TCCGTTTCGA ATCTAGTAAA GGGATATTTT GAAGTTTAAT   | 2280 |
| AGCGCTGTTT AACACTAGAA TCTCTTATAA AACAATTGAC ACAAATTTAA ATTCAACAAA  | 2340 |
| CACCGTTCTC ATGCAATTG ATCATGTTGT AAAGAACATT TCGGAATGTT ATAAATCTGC   | 2400 |
| TTTTAAGGAT CTATCAATTA ATGTTACGCA AAATATGCAA TTTTCATTCGT TCTTACAACG | 2460 |
| CATCATTGAA ATGACAGTCA GCGGTTGTCC AATTACGAAA TGTGATCCTT TAATCGAGTA  | 2520 |
| TGAGGTACGA TTCACCATAT TGAATGGATT TTTGGAAAGC CTATCTTCAA ACACATCATA  | 2580 |
| ATTAAAGAT AATATCATTC TTTTGAGAAA GGAAATTCAA CACTTGCAAG C            | 2631 |

## (2) INFORMATION FOR SEQ ID NO:226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Phe | Tyr | Cys | Thr | Glu | Ile | Ser | Ser | Thr | Val | Thr | Ile | Val | Tyr | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | His | Asp | Thr | Trp | Asn | Lys | Leu | Ile | Thr | Pro | Phe | Ile | Val | Glu | Tyr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Phe | Lys | Thr | Tyr | Leu | Val | Glu | Asn | Asn | Val | Cys | Arg | Asn | His | Asn | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Thr | Leu | Ser | Asn | Phe | Asn | His | Ser | Lys | Met | Arg | Ile | Ile | Pro | Lys |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Lys Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala  
 65 70 75 80  
 Asp Glu Glu Glu Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile  
 85 90 95  
 Gln Pro Thr Gln Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr  
 100 105 110  
 Ser Phe Thr Lys Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys  
 115 120 125  
 Glu Phe Lys Gln Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu  
 130 135 140  
 Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr  
 1 5 10 15  
 Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp  
 20 25 30  
 Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu  
 35 40 45  
 Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro  
 50 55 60  
 Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val  
 65 70 75 80  
 Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu  
 85 90 95  
 Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp  
 100 105 110  
 Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr  
 115 120 125  
 Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe  
 130 135 140  
 Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp  
 145 150 155



## (2) INFORMATION FOR SEQ ID NO:228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Lys His Lys Glu Gly Ser Gln Ile Phe Tyr Tyr Arg Lys Pro Ile Trp
1 5 10 15
Lys Leu Val Ser Lys Leu Thr Ile Val Lys Val Arg Ile Gln Phe Ser
20 25 30
Glu Lys Asn Lys Gln Met Lys Asn Asn Phe Tyr Gln Lys Ile Gln Leu
35 40 45
Glu Glu Glu Asn Leu Glu Lys Val Glu Glu Lys Leu Ile Pro Glu Asp
50 55 60
Ser Phe Gln Lys Tyr Pro Gln Gly Lys Leu Arg Ile Ile Pro Lys Lys
65 70 75 80
Gly Ser Phe Arg Pro Ile Met Thr Phe Leu Arg Lys Asp Lys Gln Lys
85 90 95
Asn Ile Lys Leu Asn Leu Asn Gln Ile Leu Met Asp Ser Gln Leu Val
100 105 110
Phe Arg Asn Leu Lys Asp Met Leu Gly Gln Lys Ile Gly Tyr Ser Val
115 120 125
Phe Asp Asn Lys Gln Ile Ser Glu Lys Phe Ala Gln Phe Ile Glu Lys
130 135 140
Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu
145 150 155

```

## (2) INFORMATION FOR SEQ ID NO:229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Tyr Tyr Tyr Arg Lys
1 5

```

## (2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Gly Lys Leu Arg Ile Ile Pro Lys Lys  
 1 5

## (2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Phe Arg Pro Ile Met Thr Phe  
 1 5

## (2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe  
 1 5 10 15

Tyr Arg Lys Ser Val Trp Ser Lys  
 20

## (2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```
Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu
1 5 10 15
Val Arg Gln His Arg Glu Ala
 20
```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```
Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg
1 5 10 15
Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
 20 25
```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```
Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
1 5 10 15
Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln
 20 25
```

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly  
 1 5 10 15  
 Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser  
 20 25 30

## (2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly  
 1 5 10 15  
 Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
 20 25

## (2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

YARACHAARG GHATYCCHYA RGG

23

## (2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Gln Thr Lys Gly Ile Pro Gln Gly  
 1 5

## (2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Asp Asp Tyr Leu Leu Ile Thr  
 1 5

## (2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

NGTNATDARD ARRTARTCRT C

21

## (2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe  
 1 5 10 15

Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu  
 20 25 30

Ser Met Asn Pro Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr  
 35 40 45

Asp Asp Tyr Leu Leu Ile Thr  
 50 55

## (2) INFORMATION FOR SEQ ID NO:243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile  
 1                      5                      10                      15

Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg  
                     20                      25                      30

Val Val

## (2) INFORMATION FOR SEQ ID NO:244:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile Val Asp Leu  
 1                      5                      10                      15

Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys Ala Ser Pro  
                     20                      25                      30

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile  
                     35                      40                      45

Ser

## (2) INFORMATION FOR SEQ ID NO:245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Gln Lys Val Gly Ile Pro Gln Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

CAAAAAGTTG GTATCCCTCA GGG

23

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

AGACCAAAGG AATTCATCA GGCTCAATTC TGTCATCTTT TTTGTGTCAT TTCTATATGG

60

AAGATTTGAT TGATGAATAC CTATCGTTTA CGAAAAAGAA AGGATCAAGT TTGTTACGAG

120

TAGTCGACGA CTACCTCCTC ATCACC

146

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Lys Gly Ile Pro Ser Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe  
1 5 10 15

Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys  
20 25 30

Gly Ser Val Leu Leu Arg Val Val Asp Asp Tyr Leu Leu Ile Thr  
 35 40 45

## (2) INFORMATION FOR SEQ ID NO:249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GACGATTTC TCTTTATAAC A

21

## (2) INFORMATION FOR SEQ ID NO:250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Asp Asp Phe Leu Phe Ile Thr  
 1 5

## (2) INFORMATION FOR SEQ ID NO:251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif 0 peptide from  
 Schizosaccharomyces pombe tezip"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr  
 1 5 10 15



Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe Arg Lys  
           20                          25                          30

Asp Ile Trp  
           35

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from  
 Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Ala Val Ile Arg Leu Leu Pro Lys Lys Asn Thr Phe Arg Leu Ile Thr  
   1                  5                          10                          15  
 Asn Leu Arg Lys Arg Phe  
                   20

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 3(A) peptide from  
 Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile  
   1                  5                          10                          15  
 Lys Gln Asp Leu Met Phe Arg Ile Val Lys  
                   20                          25

## (2) INFORMATION FOR SEQ ID NO:254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 4(B') peptide from Schizosaccharomyces pombe tezlp"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe
1 5 10 15

Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe
20 25 30

```

## (2) INFORMATION FOR SEQ ID NO:255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Schizosaccharomyces pombe tezlp"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys
1 5 10 15

Lys Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys
20 25 30

His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn
35 40 45

Ser

```

## (2) INFORMATION FOR SEQ ID NO:256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif 0 peptide from  
Saccharomyces cerevisiae EST2p"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr  
 1                      5                      10                      15  
 Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp  
                     20                      25                      30  
 Thr Trp

## (2) INFORMATION FOR SEQ ID NO:257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from  
Saccharomyces cerevisiae EST2p"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu Phe Arg Ile  
 1                      5                      10                      15  
 Ile Ala Ile Pro Cys Arg Gly Ala Asp  
                     20                      25

## (2) INFORMATION FOR SEQ ID NO:258:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```

Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile
1 5 10 15
Pro Arg Met Glu Cys Met Arg Ile Leu Lys
 20 25

```

## (2) INFORMATION FOR SEQ ID NO:259:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 4(B') peptide from  
Saccharomyces cerevisiae EST2p"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```

Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro
1 5 10 15
Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe
 20 25 30

```

## (2) INFORMATION FOR SEQ ID NO:260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: /note= "motif 5(C) peptide from  
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln
1 5 10 15
Gln Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys
20 25 30
Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala Val Ser Ser Gln
35 40 45

```

Ser

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: /note= "motif 0 peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

```

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr
1 5 10 15
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys
20 25 30
Asn Ile Trp
35

```

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..23

(D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Leu | Arg | Leu | Ile | Pro | Lys | Lys | Thr | Thr | Phe | Arg | Pro | Ile | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Thr | Phe | Asn | Lys | Lys | Ile | Val |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /note= "motif 3(A) peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Leu | Phe | Phe | Ala | Thr | Met | Asp | Ile | Glu | Lys | Cys | Tyr | Asp | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn | Arg | Glu | Lys | Leu | Ser | Thr | Phe | Leu | Lys |     |     |     |     |     |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 4(B') peptide from Euplotes aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile  
 1                      5                      10                      15

Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe  
                     20                      25                      30

## (2) INFORMATION FOR SEQ ID NO:265:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Euplotes aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu  
 1                      5                      10                      15

Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu  
                     20                      25                      30

Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro Leu  
                     35                      40                      45

Ser

## (2) INFORMATION FOR SEQ ID NO:266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 22..1716

(D) OTHER INFORMATION: /note= "EcoRI-NotI insert of  
clone 712562 encoding 63 kDa  
telomerase protein"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

|                |            |            |            |            |            |      |
|----------------|------------|------------|------------|------------|------------|------|
| GCCAAGTTCC TGC | ACTGGCT    | GATGAGTGTG | TACGTCGTCG | AGCTGCTCAG | GTCTTTCTTT | 60   |
| TATGTCACGG     | AGACCACGTT | TCAAAAGAAC | AGGCTCTTTT | TCTACCGGAA | GAGTGTCTGG | 120  |
| AGCAAGTTGC     | AAAGCATTGG | AATCAGACAG | CACTTGAAGA | GGGTGCAGCT | GCGGGAGCTG | 180  |
| TCGGAAGCAG     | AGGTCAGGCA | GCATCGGGAA | GCCAGGCCCG | CCCTGCTGAC | GTCCAGACTC | 240  |
| CSCTTCATCC     | CCAAGCCTGA | CGGGCTGCGG | CCGATTGTGA | ACATGGACTA | CGTCGTGGGA | 300  |
| GCCAGAACGT     | TCCGCAGAGA | AAAGARGGCC | GAGCGTCTCA | CCTCGAGGGT | GAAGGCACTG | 360  |
| TTCAGCGTGC     | TCAACTACGA | GCGGGCGCGG | CGCCCCGGCC | TCCTGGGCGC | CTCTGTGCTG | 420  |
| GGCCTGGACG     | ATATCCACAG | GGCCTGGCGC | ACCTTCGTGC | TGCGTGTGCG | GGCCCAGGAC | 480  |
| CTGCGCGCTG     | AGCTGTACTT | TGTCAAGGTG | GATGTGACGG | GCGCGTACGA | CACCATCCCC | 540  |
| CAGCAGAGGC     | TCACGGAGGT | CATCGCCAGC | ATCATCAAAC | CCCAGAACAC | GTA        | 600  |
| CGTCGGTATG     | CCGTGGTCCA | GAAGGCCGCC | ATGGGCACGT | CCGCAAGGCC | TTCAAGAGCC | 660  |
| AGCTCCTACG     | TCCAGTGCCA | GGGGATCCCG | CAGGGCTCCA | TCCTCTCCAC | GCTGCTCTGC | 720  |
| ATCTCTGTGT     | ACGGCGACAT | GGAGAACAAG | CTGTTTGCGG | GGATTGGGGG | GGACGGGCTG | 780  |
| CTCTCTGGGT     | TGGTGGATGA | TTTCTTGTTG | GTGACACCTC | ACCTCACCCA | CGCGAAAACC | 840  |
| TTCTCAGGA      | CCCTGGTCCG | AGGTGTCCCT | GAGTATGGCT | GCGTGGTGAA | CTTGCGGAAG | 900  |
| ACA            | GTGGTGA    | ACTTCCCTGT | AGAAGACGAG | GCCCTGGGTG | GCACGGCTTT | 960  |
| CGGGCCACG      | GCCTATTCCC | CTGGTGCGGC | CTGCTGCTGG | ATACCCGGAC | CCTGGAGGTG | 1020 |
| CAGAGCGACT     | ACTCCAGCTA | TGCCCCGACC | TCCATCAGAG | CCAGTCTCAC | CTTCAACCGC | 1080 |
| GGCTTCAAGG     | CTGGGAGGAA | CATGCGTCGC | AAACTCTTTG | GGGTCTTGCG | GCTGAAGTGT | 1140 |
| CACAGCCTGT     | TTCTGGATTT | GCAGGTGAAC | AGCCTCCAGA | CGGTGTGCAC | CAACATCTAC | 1200 |
| AAGATCCTCC     | TGCTGCAGGC | GTACAGGTTT | CACGCATGTG | TGCTGCAGCT | CCCATTTTAT | 1260 |
| CAGCAAGTTT     | GGAAGAACCC | ACATTTTTTC | TGCGCGTCAT | CTCTGACACG | GCTCCCTCTG | 1320 |
| CTACTCCATC     | CTGAAAGCCA | AGAACGCAGG | GATGTCGCTG | GGGGCCAAGG | GCGCCGCCGG | 1380 |
| CCCTCTGCCC     | TCCGAGGCCG | TGCAGTGGCT | GTGCCACCAA | GCATTCCTGC | TCAAGCTGAC | 1440 |
| TCGACACCGT     | GTCACCTACG | TGCCACTCCT | GGGGTCACTC | AGGACAGCCC | AGACGCAGCT | 1500 |
| GAGTCGGAAG     | CTCCCGGGGA | CGACGCTGAC | TGCCCTGGAG | GCCGCAGCCA | ACCCGGCACT | 1560 |



```

GCCCTCAGAC TTCAAGACCA TCCTGGACTG ATGGCCACCC GCCACAGCC AGGCCGAGAG 1620
CAGACACCAG CAGCCCTGTC ACGCCGGGCT TATACGTCCC AGGGAGGGAG GGGCGGCCCCA 1680
CACCCAGGCC TGCACCGCTG GGAGTCTGAG GCCTGAGTGA GTGTTTGGCC GAGGCCTGCA 1740
TGTCCGGCTG AAGGCTGAGT GTCCGGCTGA GGCCTGAGCG AGTGTCCAGC CAAGGGCTGA 1800
GTGTCCAGCA CACCTGCGTT TTTACTTCCC CACAGGCTGG CGTTCGGTCC ACCCCAGGGC 1860
CAGCTTTTCC TCACCAGGAG CCCGGCTTCC ACTCCCCACA TAGGAATAGT CCATCCCCAG 1920
ATTGCGCCATT GTTCACCCTT CGCCCTGCCT TCCTTTGCCT TCCACCCCCA CCATTCAGGT 1980
GGAGACCCTG AGAAGGACCC TGGGAGCTTT GGGAAATTGG AGTGACCAAA GGTGTGCCCT 2040
GTACACAGGC GAGGACCCTG CACCTGGATG GGGGTCCCTG TGGGTCAAAT TGGGGGGAGG 2100
TGCTGTGGGA GTAAAATACT GAATATATGA GTTTTTCAGT TTTGGAAAAA AAAAAAAAAA 2160
AAAAAAAAA A 2171

```

## (2) INFORMATION FOR SEQ ID NO:267:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..564
- (D) OTHER INFORMATION: /note= "63 kDa telomerase protein encoded by ORF of EcoRI-NotI insert of clone 712562"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```

Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr
1 5 10 15
Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val
20 25 30
Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val
35 40 45
Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala
50 55 60
Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp
65 70 75 80
Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr
85 90 95

```

Phe Arg Arg Glu Lys Xaa Ala Glu Arg Leu Thr Ser Arg Val Lys Ala  
 100 105 110  
 Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu  
 115 120 125  
 Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr  
 130 135 140  
 Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe  
 145 150 155 160  
 Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg  
 165 170 175  
 Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys  
 180 185 190  
 Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala Met Gly Thr Ser Ala  
 195 200 205  
 Arg Pro Ser Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln  
 210 215 220  
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met  
 225 230 235 240  
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg  
 245 250 255  
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys  
 260 265 270  
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val  
 275 280 285  
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala  
 290 295 300  
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro  
 305 310 315 320  
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp  
 325 330 335  
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn  
 340 345 350  
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val  
 355 360 365  
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser  
 370 375 380  
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala  
 385 390 395 400  
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val  
 405 410 415

Trp Lys Asn Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg Leu Pro  
                     420                    425                    430  
 Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp Val Ala Gly Gly  
                     435                    440                    445  
 Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg Ala Val Ala Val  
                     450                    455                    460  
 Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro Cys His Leu Arg  
                     465                    470                    475                    480  
 Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala Ala Glu Ser Glu  
                     485                    490                    495  
 Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg Ser Gln Pro Gly  
                     500                    505                    510  
 Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met Ala Thr Arg Pro  
                     515                    520                    525  
 Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser Arg Arg Ala Tyr  
                     530                    535                    540  
 Thr Ser Gln Gly Gly Arg Gly Gly Pro His Pro Gly Leu His Arg Trp  
                     545                    550                    555                    560  
 Glu Ser Glu Ala

## (2) INFORMATION FOR SEQ ID NO:268:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from  
Euplotes aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln  
 1                    5                    10                    15  
 Lys Ser Tyr Ser Lys Thr  
                     20

## (2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..30
  - (D) OTHER INFORMATION: /note= "motif 0 peptide from Euplotes aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ser | Leu | Gly | Phe | Ala | Pro | Gly | Lys | Leu | Arg | Leu | Ile | Pro | Lys | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Thr | Thr | Phe | Arg | Pro | Ile | Met | Thr | Phe | Asn | Lys | Lys | Ile | Val |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

## (2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..27
  - (D) OTHER INFORMATION: /note= "motif A peptide from Euplotes aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Leu | Phe | Phe | Ala | Thr | Met | Asp | Ile | Glu | Lys | Cys | Tyr | Asp | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Asn | Arg | Glu | Lys | Leu | Ser | Thr | Phe | Leu | Lys |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gly | Lys | Phe | Tyr | Lys | Gln | Thr | Lys | Gly | Ile | Pro | Gln | Gly | Leu | Cys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Ser | Ser | Ile | Leu | Ser | Ser | Phe | Tyr | Tyr | Ala |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 22
- (D) OTHER INFORMATION: /note= "motif C peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Asn | Val | Asn | Leu | Leu | Met | Arg | Leu | Thr | Asp | Asp | Tyr | Leu | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Thr | Gln | Glu | Asn | Asn |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from  
Euplotes aediculatus p123"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:274:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from  
Schizosaccharomyces pombe tez1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser  
 1                      5                      10                      15

Asp Leu Arg Asn Arg Thr  
 20

## (2) INFORMATION FOR SEQ ID NO:275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "motif 0 peptide from  
Schizosaccharomyces pombe tez1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys  
 1                      5                      10                      15  
 Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu  
                     20                      25                      30

## (2) INFORMATION FOR SEQ ID NO:276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from  
 Schizosaccharomyces pombe tez1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg  
 1                      5                      10                      15  
 Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys  
                     20                      25

## (2) -INFORMATION FOR SEQ ID NO:277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from  
 Schizosaccharomyces pombe tez1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile  
 1                      5                      10                      15  
 Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu  
                     20                      25

## (2) INFORMATION FOR SEQ ID NO:278:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from  
Schizosaccharomyces pombe tez1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile  
 1                      5                      10                      15

Thr Val Asn Lys Lys Asp  
                     20

## (2) INFORMATION FOR SEQ ID NO:279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from  
Schizosaccharomyces pombe tez1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His Asn Phe Ser Thr  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:280:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide



## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from  
Saccharomyces cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr Glu Ile Ser
1 5 10 15
Ser Thr Val Thr Ile Val
 20

```

## (2) INFORMATION FOR SEQ ID NO:281:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "motif 0 peptide from  
Saccharomyces cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```

Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys
1 5 10 15
Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp
 20 25 30

```

## (2) INFORMATION FOR SEQ ID NO:282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser  
 1                   5                   10                   15  
 Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys  
                   20                   25

## (2) INFORMATION FOR SEQ ID NO:283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from  
Saccharomyces cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Glu Asp Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser  
 1                   5                   10                   15  
 Leu Ser Ala Pro Ile Val Asp Leu Val Tyr Asp  
                   20                   25

## (2) INFORMATION FOR SEQ ID NO:284:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from  
Saccharomyces cerevisiae EST2"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile  
 1                   5                   10                   15  
 Ser Thr Asp Gln Gln Gln  
                   20

## (2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..15
  - (D) OTHER INFORMATION: /note= "motif D peptide from  
Saccharomyces cerevisiae EST2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE-CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..22
  - (D) OTHER INFORMATION: /note= "motif 1 peptide from human  
telomerase core protein 1 (TCPI)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr  
 1                      5                      10                      15

Phe Gln Lys Asn Arg Leu  
 20

## (2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "motif 0 peptide from human telomerase core protein 1 (TCP1)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 1                      5                      10                      15

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly  
                     20                      25                      30

## (2) INFORMATION FOR SEQ ID NO:288:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from human telomerase core protein 1 (TCP1)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr-  
 1                      5                      10                      15

Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala  
                     20                      25

## (2) INFORMATION FOR SEQ ID NO:289:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from human telomerase core protein 1 (TCP1)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile  
 1                      5                      10                      15  
 Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly  
                     20                      25

## (2) INFORMATION FOR SEQ ID NO:290:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from human  
telomerase core protein 1 (TCP1)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val  
 1                      5                      10                      15  
 Thr Pro His Leu Thr His  
                     20

## (2) INFORMATION FOR SEQ ID NO:291:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from human  
telomerase core protein 1 (TCP1)"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:292:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..4029
- (D) OTHER INFORMATION: /note= "preliminary sequence for human TRT cDNA insert of plasmid pGRN121"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCGATGCC 60
GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC AGCCACTACC GCGAGGTGCT 120
GCCGCTGGCC ACGTTCGTGC GGC GCCTGGG GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG 180
GGACCCGGCG GCTTTCGCG CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN 240
ANGGCGNGCC CCGCGCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC 300
CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT TCGGCTTCGC 360
GCTGCTGGAC GGGGCCCCGCG GGGGCCCCCC CGAGGCCTTC ACCACCAGCG TGCGCAGCTA 420
CCTGCCCAAC ACGGTGACCG ACGCACTGCG GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG 480
CGCGGTGGGC GACGACGTGC TGGTTCACCT GCTGGCACGC TCGCGGNTNT TGTGCTGGT 540
GGHTCCCAGC TCGCGCTACC ANGTTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC 600
TCAGGCCCCG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC CAACGGGCCT 660
GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG CCAGCCCCCG GTGCGAGGAG 720
GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC 780
CCCTGAGCCG GAGCGGACGC CCGTTGGGCA GGGGTCCTGG GCCCACC CGG GCAGGACGCC 840
TGGACCGAGT GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC 900
CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG GCCGCCAGCA 960
CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT GGGACACGCC TTGTCCCCCG 1020
GTGTACGCCG AGACCAAGCA CTTCTCTTAC TCCTCAGGCG ACAAGNACAC TGCGNCCCTC 1080
CTTCCTACTC AATATATCTG AGGCCCAGCC TGA CTGGCGT TCGGGAGGTT CGTGGAGACA 1140
NTCTTTCTGG TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA 1200

```

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGAACCCACG CGCAGTGCCC | 1260 |
| CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT GCGGTCACCC CAGCAGCCGG | 1320 |
| TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC TGTGGCGGCC CCCGAGGAGG AGGAACACAG | 1380 |
| ACCCCCGTGC CCTGGTGCAG CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT | 1440 |
| TCGTGCGGGC CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG | 1500 |
| AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT GCCAAGCTCT | 1560 |
| CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG CGCTTGGCTG CGCAGGAGCC | 1620 |
| CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC ACCGTCTGCG TGAGGAGATC CTGGCCAAGT | 1680 |
| TCCTGCACTG GCTGATGAGT GTGTACGTGC TCGAGCTGCT CAGGTCTTTC TTTTATGTCA | 1740 |
| CGGAGACCAC GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT | 1800 |
| TGCAAAGCAT TGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG CTGTCGGAAG  | 1860 |
| CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT GACGTCCAGA CTCCGCTTCA | 1920 |
| TCCCCAAGCC TGACGGGCTG CGGCCGATTG TGAACATGGA CTACGTCTGT GGAGCCAGAA | 1980 |
| CGTTCCGCAG AGAAAAGAGG GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTACGCG | 2040 |
| TGCTCAACTA CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG | 2100 |
| ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG GACCCGCCGC | 2160 |
| CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA CGACACCATC CCCCAGGACA | 2220 |
| GGCTCACGGA GGTTCATCGC AGCATCATCA ACCCCAGAA CACGTA CTGC            | 2280 |
| ATGCCGTGGT CCAGAAGGCC GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT | 2340 |
| CTACCTTGAC AGACCTCCAG CCGTACATGC GACAGTTCTG GGCTCACCTG CAGGANAACA | 2400 |
| GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG GCCAGCAGTG | 2460 |
| GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC CGTGCGCATC AGGGGCAAGT | 2520 |
| CCTACGTCCA GTGCCAGGGG ATCCCGCAGG GCTCCATCCT CTCCACGCTG CTCTGCAGCC | 2580 |
| TGTGCTACGG CGACATGGAG AACAACTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC  | 2640 |
| TGCGTTTGGT GGATGATTTT TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC | 2700 |
| TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG CGGAAGACAG | 2760 |
| TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC GGCTTTTGTT CAGATGCCGG | 2820 |
| CCCACGGCCT ATTCCCCTGG TGCGGCCTGC TGCTGGATAC CCGGACCCTG GAGGTGCAGA | 2880 |
| GCGACTACTC CAGCTATGCC CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT | 2940 |
| TCAAGGCTGG GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCA   | 3000 |
| GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC ATCTACAAGA | 3060 |

```

TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT GCAGCTCCCA TTTCATCAGC 3120
AAGTTTGGA GAACCCACACA TTTTTCCTGC GCGTCATCTC TGACACGGCC TCCCTCTGCT 3180
ACTCCATCCT GAAAGCCAAG AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC 3240
CTCTGCCCTC CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC 3300
GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACCTCAG GACAGCCCAG ACGCAGCTGA 3360
GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC CGCAGCCAAC CCGGCACTGC 3420
CCTCAGACTT CAAGACCATC CTGGACTGAT GGCCACCCGC CCACAGCCAG GCCGAGAGCA 3480
GACACCAGCA GCCCTGTCAC GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCCACAC 3540
CCAGGCCCCG ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT 3600
CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA GGGCTGAGTG 3660
TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG CTCGGCTCCA CCCAGGGCC 3720
AGCTTTTCCT CACCAGGAGC CCGGCTTCCA CTCCCCACAT AGGAATAGTC CATCCCCAGA 3780
TTGCCCATTG TTCACCCCTC GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG 3840
GAGACCCTGA GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG 3900
TACACAGGCG AGGACCCTGC ACCTGGATGG GGTCCCTGT GGGTCAAATT GGGGGGAGGT 3960
GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT TTGAAAAAA AAAAAAAAAA 4020
AAAAAAAAA 4029

```

## (2) INFORMATION FOR SEQ ID NO:293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```

Ala Ala Leu Arg Pro Ala Ala His Val Gly Ser Pro Gly Pro Gly His
1 5 10 15
Pro Arg Asp Ala Ala Arg Ser Pro Leu Pro Ser Arg Ala Leu Pro Ala
20 25 30
Ala Gln Pro Leu Pro Arg Gly Ala Ala Ala Gly His Val Arg Ala Ala
35 40 45
Pro Gly Ala Pro Gly Leu Ala Ala Gly Ala Ala Arg Gly Pro Gly Gly
50 55 60

```



Phe Pro Arg Xaa Gly Gly Pro Xaa Xaa Gly Val Arg Ala Leu Gly Xaa  
 65 70 75 80  
 Xaa Ala Ala Pro Arg Arg Pro Leu Leu Pro Pro Gly Val Leu Pro Glu  
 85 90 95  
 Xaa Xaa Gly Gly Pro Ser Ala Ala Xaa Ala Val Arg Xaa Arg Arg Glu  
 100 105 110  
 Xaa Arg Ala Gly Leu Arg Leu Arg Ala Ala Gly Arg Gly Pro Arg Gly  
 115 120 125  
 Pro Pro Arg Gly Leu His His Gln Arg Ala Gln Leu Pro Ala Gln His  
 130 135 140  
 Gly Asp Arg Arg Thr Ala Gly Glu Arg Gly Val Gly Ala Ala Ala Ala  
 145 150 155 160  
 Pro Arg Gly Arg Arg Arg Ala Gly Ser Pro Ala Gly Thr Leu Arg Xaa  
 165 170 175  
 Xaa Cys Ala Gly Gly Ser Gln Leu Arg Leu Pro Xaa Val Arg Ala Ala  
 180 185 190  
 Ala Val Pro Ala Arg Arg Cys Xaa Ser Gly Pro Ala Pro Ala Thr Arg  
 195 200 205  
 Xaa Trp Thr Arg Xaa Arg Leu Gly Ser Asn Gly Pro Gly Thr Ile Ala  
 210 215 220  
 Ser Gly Arg Pro Gly Ser Pro Trp Ala Ala Ser Pro Gly Cys Glu Glu  
 225 230 235 240  
 Ala Arg Gly Gln Cys Gln Pro Lys Ser Ala Val Ala Gln Glu Ala Gln  
 245 250 255  
 Ala Trp Arg Cys Pro  
 260

## (2) INFORMATION FOR SEQ ID NO:294:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Ala Gly Ala Asp Ala Arg Trp Ala Gly Val Leu Gly Pro Pro Gly Gln  
 1 5 10 15  
 Asp Ala Trp Thr Glu  
 20

## (2) INFORMATION FOR SEQ ID NO:295:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```

Pro Trp Phe Leu Cys Gly Val Thr Cys Gln Thr Arg Arg Arg Ser His
1 5 10 15
Leu Phe Gly Gly Cys Ala Leu Trp His Ala Pro Leu Pro Pro Ile Arg
 20 25 30
Gly Pro Pro Ala Pro Arg Gly Pro Pro Ile His Ile Ala Ala Thr Thr
 35 40 45
Ser Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe
 50 55 60
Leu Tyr Ser Ser Gly Asp Lys Xaa Thr Ala Xaa Leu Leu Pro Thr Gln
65 70 75 80
Tyr Ile

```

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```

Leu Ala Phe Gly Arg Phe Val Glu Thr Xaa Phe Leu Val Pro Gly Leu
1 5 10 15
Gly Cys Gln Asp Ser Pro Gln Val Ala Pro Pro Ala Pro Ala Xaa Leu
 20 25 30
Ala Asn Ala Ala Pro Val Ser Gly Ala Ala Trp Glu Pro Arg Ala Val
 35 40 45
Pro Leu Arg Gly Val Pro Gln Asp Ala Leu Pro Ala Ala Ser Cys Gly
 50 55 60
His Pro Ser Ser Arg Cys Leu Cys Pro Gly Glu Ala Pro Gly Leu Cys
65 70 75 80
Gly Gly Pro Arg Gly Gly Gly Thr Gln Thr Pro Val Ala Trp Cys Ser
 85 90 95

```

Cys Ser Ala Ser Thr Ala Ala Pro Gly Arg Cys Thr Ala Ser Cys Gly  
                   100                  105                  110

Pro Ala Cys Ala Gly Trp Cys Pro Gln Ala Ser Gly Ala Pro Gly Thr  
                   115                  120                  125

Thr Asn Ala Ala Ser Ser Gly Thr Pro Arg Ser Ser Ser Pro Trp Gly  
           130                  135                  140

Ser Met Pro Ser Ser Arg Cys Arg Ser  
   145                  150

## (2) INFORMATION FOR SEQ ID NO:297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Ala Cys Gly Thr Ala Leu Gly Cys Ala Gly Ala Gln Gly Leu Ala Val  
   1                  5                  10                  15

Phe Arg Pro Gln Ser Thr Val Cys Val Arg Arg Ser Trp Pro Ser Ser  
           20                  25                  30

Cys Thr Gly  
           35

## (2) INFORMATION FOR SEQ ID NO:298:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Val Cys Thr Ser Ser Ser Cys Ser Gly Leu Ser Phe Met Ser Arg Arg  
   1                  5                  10                  15

Pro Arg Phe Lys Arg Thr Gly Ser Phe Ser Thr Gly Arg Val Ser Gly  
           20                  25                  30

Ala Ser Cys Lys Ala Leu Glu Ser Asp Ser Thr  
           35                  40

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Arg Gly Cys Ser Cys Gly Ser Cys Arg Lys Gln Arg Ser Gly Ser Ile  
1 5 10 15  
Gly Lys Pro Gly Pro Pro Cys  
20

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Arg Pro Asp Ser Ala Ser Ser Pro Ser Leu Thr Gly Cys Gly Arg Leu  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Thr Trp Thr Thr Ser Trp Glu Pro Glu Arg Ser Ala Glu Lys Arg Gly  
1 5 10 15  
Pro Ser Val Ser Pro Arg Gly  
20

## (2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Arg His Cys Ser Ala Cys Ser Thr Thr Ser Gly Arg Gly Ala Pro Ala
1 5 10 15

Ser Trp Ala Pro Leu Cys Trp Ala Trp Thr Ile Ser Thr Gly Pro Gly
 20 25 30

Ala Pro Ser Cys Cys Val Cys Gly Pro Arg Thr Arg Arg Leu Ser Cys
 35 40 45

Thr Leu Ser Arg Trp Met
 50

```

## (2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

Arg Ala Arg Thr Thr Pro Ser Pro Arg Thr Gly Ser Arg Arg Ser Ser
1 5 10 15

Pro Ala Ser Ser Asn Pro Arg Thr Arg Thr Ala Cys Val Gly Met Pro
 20 25 30

Trp Ser Arg Arg Pro Pro Met Gly Thr Ser Ala Arg Pro Ser Arg Ala
 35 40 45

Thr Ser Leu Pro
 50

```

## (2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Gln Thr Ser Ser Arg Thr Cys Asp Ser Ser Trp Leu Thr Cys Arg Xaa  
 1                      5                      10                      15

Thr Ala Arg

## (2) INFORMATION FOR SEQ ID NO:305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Gly Met Pro Ser Ser Ser Ser Arg Ala Pro Pro  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:306:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Arg Pro Ala Val Ala Ser Ser Thr Ser Ser Tyr Ala Ser Cys Ala  
 1                      5                      10                      15

Thr Thr Pro Cys Ala Ser Gly Ala Ser Pro Thr Ser Ser Ala Arg Gly  
 20                      25                      30

Ser Arg Arg Ala Pro Ser Ser Pro Arg Cys Ser Ala Ala Cys Ala Thr  
 35                      40                      45

Ala Thr Trp Arg Thr Ser Cys Leu Arg Gly Phe Gly Gly Thr Gly Cys  
 50                      55                      60

Ser Cys Val Trp Trp Met Ile Ser Cys Trp  
 65                      70

## (2) INFORMATION FOR SEQ ID NO:307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

His Leu Thr Ser Pro Thr Arg Lys Pro Ser Ser Gly Pro Trp Ser Glu  
 1                      5                      10                      15  
 Val Ser Leu Ser Met Ala Ala Trp  
                     20

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Thr Cys Gly Arg Gln Trp  
 1                      5

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Lys Thr Arg Pro Trp Val Ala Arg Leu Leu Phe Arg Cys Arg Pro Thr  
 1                      5                      10                      15  
 Ala Tyr Ser Pro Gly Ala Ala Cys Cys Trp Ile Pro Gly Pro Trp Arg  
                     20                      25                      30  
 Cys Arg Ala Thr Thr Pro Ala Met Pro Gly Pro Pro Ser Glu Pro Val  
                     35                      40                      45  
 Ser Pro Ser Thr Ala Ala Ser Arg Leu Gly Gly Thr Cys Val Ala Asn  
                     50                      55                      60  
 Ser Leu Gly Ser Cys Gly  
                     65                      70

## (2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Ser Val Thr Ala Cys Phe Trp Ile Cys Arg  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Thr Ala Ser Arg Arg Cys Ala Pro Thr Ser Thr Arg Ser Ser Cys Cys  
 1                      5                      10                      15

Arg Arg Thr Gly Phe Thr His Val Cys Cys Ser Ser His Phe Ile Ser  
 20                      25                      30

Lys Phe Gly Arg Thr Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg  
 35                      40                      45

Pro Pro Ser Ala Thr Pro Ser  
 50                      55

## (2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Lys Pro Arg Thr Gln Gly Cys Arg Trp Gly Pro Arg Ala Pro Pro Ala  
 1                      5                      10                      15



Leu Cys Pro Pro Arg Pro Cys Ser Gly Cys Ala Thr Lys His Ser Cys  
                   20                  25                  30

Ser Ser

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Leu Asp Thr Val Ser Pro Thr Cys His Ser Trp Gly His Ser Gly Gln  
 1                  5                  10                  15  
 Pro Arg Arg Ser  
                   20

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Val Gly Ser Ser Arg Gly Arg Arg  
 1                  5

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Leu Pro Trp Arg Pro Gln Pro Thr Arg His Cys Pro Gln Thr Ser Arg  
 1                  5                  10                  15  
 Pro Ser Trp Thr Asp Gly His Pro Pro Thr Ala Arg Pro Arg Ala Asp  
                   20                  25                  30

Thr Ser Ser Pro Val Thr Pro Gly Ser Thr Ser Gln Gly Gly Arg Gly  
 35 40 45

Gly Pro His Pro Gly Pro His Arg Trp Glu Ser Glu Ala  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Val Ser Val Trp Pro Arg Pro Ala Cys Pro Ala Glu Gly  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Gly Leu Ser Glu Cys Pro Ala Lys Gly  
 1 5

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Val Ser Ser Thr Pro Ala Val Phe Thr Ser Pro Gln Ala Gly Ala Arg  
 1 5 10 15

Leu His Pro Arg Ala Ser Phe Ser Ser Pro Gly Ala Arg Leu Pro Leu  
 20 25 30

Pro Thr

## (2) INFORMATION FOR SEQ ID NO:319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```

Ser Ile Pro Arg Phe Ala Ile Val His Pro Ser Pro Cys Pro Pro Leu
1 5 10 15

Pro Ser Thr Pro Thr Ile Gln Val Glu Thr Leu Arg Arg Thr Leu Gly
 20 25 30

Ala Leu Gly Ile Trp Ser Asp Gln Arg Cys Ala Leu Tyr Thr Gly Glu
 35 40 45

Asp Pro Ala Pro Gly Trp Gly Ser Leu Trp Val Lys Leu Gly Gly Gly
 50 55 60

Ala Val Gly Val Lys Tyr
 65 70

```

## (2) INFORMATION FOR SEQ ID NO:320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```

Ile Tyr Glu Phe Phe Ser Phe Glu Lys Lys Lys Lys Lys Lys Lys
1 5 10 15

```

## (2) INFORMATION FOR SEQ ID NO:321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```

Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala Thr
1 5 10 15

```

Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu  
 20 25 30  
 Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg  
 35 40 45  
 Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala  
 50 55 60  
 Phe Arg Ala Xaa Val Ala Xaa Cys Xaa Val Cys Val Pro Trp Xaa Xaa  
 65 70 75 80  
 Xaa Xaa Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Xaa  
 85 90 95  
 Xaa Leu Val Ala Arg Val Leu Xaa Xaa Leu Cys Xaa Arg Gly Ala Xaa  
 100 105 110  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 115 120 125  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 130 135 140  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 145 150 155 160  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Xaa  
 165 170 175  
 Phe Val Leu Val Xaa Pro Ser Cys Ala Tyr Xaa Val Cys Gly Pro Pro  
 180 185 190  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
 195 200 205  
 Xaa Gly Pro Glu Xaa Val Trp Asp Pro Thr Gly Leu Glu Pro  
 210 215 220

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Arg Gln Gly Gly Arg Gly Pro Pro Gly Leu Pro Ala Pro Gly Ala Arg  
 1 5 10 15  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 20 25 30  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 35 40 45

Ser Trp Ala His Pro Gly Arg Thr Pro Gly Pro Ser Asp Arg Gly Phe  
 50 55 60  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 65 70 75 80  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 85 90 95  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Gly Thr  
 100 105 110  
 Arg Leu Val Pro Arg Cys Thr Pro Arg Pro Ser Thr Ser Ser Thr Pro  
 115 120 125  
 Gln Ala Thr Xaa Thr Leu Arg Pro Ser Phe Leu Leu Asn Ile Ser Glu  
 130 135 140  
 Ala Gln Pro Asp Trp Arg Ser Gly Gly Ser Trp Arg Xaa Ser Phe Trp  
 145 150 155 160  
 Phe Gln Ala Leu Asp Ala Arg Ile Pro Arg Arg Leu Pro Arg Leu Pro  
 165 170 175  
 Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn  
 180 185 190  
 His Ala Gln Cys Pro Tyr Gly Val Phe Leu Lys Thr His Cys Pro Leu  
 195 200 205  
 Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro  
 210 215 220  
 Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Glu His Arg Pro Pro Ser  
 225 230 235 240  
 Pro Gly Ala Ala Ala Pro Pro Ala Gln Gln Pro Leu Ala Gly Val Arg  
 245 250 255  
 Leu Arg Ala Gly Leu Pro Ala Pro Ala Gly Ala Pro Arg Pro Leu Gly  
 260 265 270  
 Leu Gln Ala Gln Arg Thr Pro Leu Pro Gln Glu His Gln Glu Val His  
 275 280 285  
 Leu Pro Gly Glu Ala Cys Gln Ala Leu Ala Ala Gly Ala Asp Val Glu  
 290 295 300  
 Asp Glu Arg Ala Gly Leu Arg Leu Ala Ala Gln Glu Pro Arg Gly Trp  
 305 310 315 320  
 Leu Cys Ser Gly Arg Arg Ala Pro Ser Ala  
 325 330

## (2) INFORMATION FOR SEQ ID NO:323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Gly Asp Pro Gly Gln Val Pro Ala Leu Ala Asp Glu Cys Val Arg Arg  
 1                      5                      10                      15  
 Arg Ala Ala Gln Val Phe Leu Leu Cys His Gly Asp His Val Ser Lys  
                     20                      25                      30  
 Glu Gln Ala Leu Phe Leu Pro Glu Glu Cys Leu Glu Gln Val Ala Lys  
                     35                      40                      45  
 His Trp Asn Gln Thr Ala Leu Glu Glu Gly Ala Ala Ala Gly Ala Val  
                     50                      55                      60  
 Gly Ser Arg Gly Gln Ala Ala Ser Gly Ser Gln Ala Arg Pro Ala Asp  
                     65                      70                      75                      80  
 Val Gln Thr Pro Leu His Pro Gln Ala  
                                             85

## (2) INFORMATION FOR SEQ ID NO:324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Arg Ala Ala Ala Asp Cys Glu His Gly Leu Arg Arg Gly Ser Gln Asn  
 1                      5                      10                      15  
 Val Pro Gln Arg Lys Glu Gly Arg Ala Ser His Leu Glu Gly Glu Gly  
                     20                      25                      30  
 Thr Val Gln Arg Ala Gln Leu Arg Ala Gly Ala Ala Pro Arg Pro Pro  
                     35                      40                      45  
 Gly Arg Leu Cys Ala Gly Pro Gly Arg Tyr Pro Gln Gly Leu Ala His  
                     50                      55                      60  
 Leu Arg Ala Ala Cys Ala Gly Pro Gly Pro Ala Ala  
                     65                      70                      75

## (2) INFORMATION FOR SEQ ID NO:325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```

Ala Val Leu Cys Gln Gly Gly Cys Asp Gly Arg Val Arg His His Pro
1 5 10 15

Pro Gly Gln Ala His Gly Gly His Arg Gln His His Gln Thr Pro Glu
 20 25 30

His Val Leu Arg Ala Ser Val Cys Arg Gly Pro Glu Gly Arg Pro Trp
 35 40 45

Ala Arg Pro Gln Gly Leu Gln Glu Pro Arg Leu Tyr Leu Asp Arg Pro
 50 55 60

Pro Ala Val His Ala Thr Val Arg Gly Ser Pro Ala Gly Xaa Gln Pro
65 70 75 - 80

Ala Glu Gly Cys Arg Arg His Arg Ala Glu Leu Leu Pro Glu
 85 90

```

## (2) INFORMATION FOR SEQ ID NO:326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Gly Gln Gln Trp Pro Leu Arg Arg Leu Pro Thr Leu His Val Pro Pro
1 5 10 15

Arg Arg Ala His Gln Gly Gln Val Leu Arg Pro Val Pro Gly Asp Pro
 20 25 30

Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg
 35 40 45

His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro
 50 55 60

Ala Phe Gly Gly
65

```

## (2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Phe Leu Val Gly Asp Thr Ser Pro His Pro Arg Glu Asn Leu Pro Gln  
 1                      5                      10                      15  
 Asp Pro Gly Pro Arg Cys Pro  
                     20

## (2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Val Trp Leu Arg Gly Glu Leu Ala Glu Asp Ser Gly Glu Leu Pro Cys  
 1                      5                      10                      15  
 Arg Arg Arg Gly Pro Gly Trp His Gly Phe Cys Ser Asp Ala Gly Pro  
                     20                      25                      30  
 Arg Pro Ile Pro Leu Val Arg Pro Ala Ala Gly Tyr Pro Asp Pro Gly  
                     35                      40                      45  
 Gly Ala Glu Arg Leu Leu Gln Leu Cys Pro Asp Leu His Gln Ser Gln  
                     50                      55                      60  
 Ser His Leu Gln Pro Arg Leu Gln Gly Trp Glu Glu His Ala Ser Gln  
 65                      70                      75                      80  
 Thr Leu Trp Gly Leu Ala Ala Glu Val Ser Gln Pro Val Ser Gly Phe  
                     85                      90                      95  
 Ala Gly Glu Gln Pro Pro Asp Gly Val His Gln His Leu Gln Asp Pro  
                     100                      105                      110  
 Pro Ala Ala Gly Val Gln Val Ser Arg Met Cys Ala Ala Ala Pro Ile  
                     115                      120                      125  
 Ser Ser Ala Ser Leu Glu Glu Pro His Ile Phe Pro Ala Arg His Leu  
                     130                      135                      140



## (2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

His Gly Leu Pro Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp
1 5 10 15
Val Ala Gly Gly Gln Gly Arg Arg Arg Pro Ser Ala Leu Arg Gly Arg
20 25 30
Ala Val Ala Val Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro
35 40 45
Cys His Leu Arg Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala
50 55 60
Ala Glu Ser Glu Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg
65 70 75 80
Ser Gln Pro Gly Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met
85 90 95
Ala Thr Arg Pro Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser
100 105 110
Arg Arg Ala Leu Arg Pro Arg Glu Gly Gly Ala Ala His Thr Gln Ala
115 120 125
Arg Thr Ala Gly Ser Leu Arg Pro Glu
130 135

```

## (2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

Val Phe Gly Arg Gly Leu His Val Arg Leu Lys Ala Glu Cys Pro Ala
1 5 10 15
Glu Ala

```

## (2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Ala Ser Val Gln Pro Arg Ala Glu Cys Pro Ala His Leu Pro Ser Ser  
 1                   5                   10                   15  
 Leu Pro His Arg Leu Ala Leu Gly Ser Thr Pro Gly Pro Ala Phe Pro  
                  20                   25                   30  
 His Gln Glu Pro Gly Phe His Ser Pro His Arg Asn Ser Pro Ser Pro  
                  35                   40                   45  
 Asp Ser Pro Leu Phe Thr Pro Arg Pro Ala Leu Leu Cys Leu Pro Pro  
                  50                   55                   60  
 Pro Pro Ser Arg Trp Arg Pro  
                  65                   70

## (2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Glu Gly Pro Trp Glu Leu Trp Glu Phe Gly Val Thr Lys Gly Val Pro  
 1                   5                   10                   15  
 Cys Thr Gln Ala Arg Thr Leu His Leu Asp Gly Gly Pro Cys Gly Ser  
                  20                   25                   30  
 Asn Trp Gly Glu Val Leu Trp Glu  
                  35                   40

## (2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Asn Thr Glu Tyr Met Ser Phe Ser Val Leu Lys Lys Lys Lys Lys Lys  
 1 5 10 15  
 Lys Lys

## (2) INFORMATION FOR SEQ ID NO:334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Ser Ala Ala Ser Cys Cys Ala Arg Gly Lys Pro Trp Pro Arg Pro Pro  
 1 5 10 15  
 Pro Arg Cys Arg Ala Leu Pro Ala Ala Glu Pro Cys Ala Pro Cys Cys  
 20 25 30  
 Ala Ala Thr Thr Ala Arg Cys Cys Arg Trp Pro Arg Ser Cys Gly Ala  
 35 40 45  
 Trp Gly Pro Arg Ala Gly Gly Trp Cys Ser Ala Gly Thr Arg Arg Leu  
 50 55 60  
 Ser Ala Arg Trp Trp Pro Xaa Ala Trp Cys Ala Cys Pro Gly Xaa Xaa  
 65 70 75 80  
 Gly Xaa Pro Pro Pro Pro Pro Pro Ser Ala Arg Cys Pro Ala  
 85 90

## (2) INFORMATION FOR SEQ ID NO:335:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Xaa Xaa Trp Trp Pro Glu Cys Cys Xaa Xaa Cys Ala Xaa Ala Ala Arg  
 1 5 10 15  
 Xaa Thr Cys Trp Pro Ser Ala Ser Arg Cys Trp Thr Gly Pro Ala Gly  
 20 25 30

Arq

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Gln Xaa His Cys Xaa Pro Pro Ser Tyr Ser Ile Tyr Leu Arg Pro Ser  
210 215 220

Leu Thr Gly Val Arg Glu Val Arg Gly Asp Xaa Leu Ser Gly Ser Arg  
 225 230 235 240  
 Pro Trp Met Pro Gly Phe Pro Ala Gly Cys Pro Ala Cys Pro Ser Xaa  
 245 250 255  
 Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr Arg  
 260 265 270  
 Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu Leu  
 275 280 285  
 Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg Ala  
 290 295 300  
 Leu Trp Arg Pro Pro Arg Arg Arg Asn Thr Asp Pro Arg Arg Leu Val  
 305 310 315 320  
 Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val  
 325 330 335  
 Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg  
 340 345 350  
 His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu  
 355 360 365  
 Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser  
 370 375 380  
 Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val  
 385 390 395 400  
 Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu  
 405 410 415  
 His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe  
 420 425 430  
 Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg  
 435 440 445  
 Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu  
 450 455 460  
 Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His  
 465 470 475 480  
 Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro  
 485 490 495  
 Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly  
 500 505 510  
 Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg  
 515 520 525  
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro  
 530 535 540

Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala  
 545 550 555 560  
 Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu  
 565 570 575  
 Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro  
 580 585 590  
 Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn  
 595 600 605  
 Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly  
 610 615 620  
 His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu  
 625 630 635 640  
 Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Xaa Asn Ser Pro  
 645 650 655  
 Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala  
 660 665 670  
 Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala  
 675 680 685  
 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln  
 690 695 700  
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met  
 705 710 715 720  
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg  
 725 730 735  
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys  
 740 745 750  
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val  
 755 760 765  
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala  
 770 775 780  
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro  
 785 790 795 800  
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp  
 805 810 815  
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn  
 820 825 830  
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val  
 835 840 845  
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser  
 850 855 860

Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala  
 865 870 875 880  
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val  
 885 890 895  
 Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser  
 900 905 910  
 Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly  
 915 920 925  
 Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu  
 930 935 940  
 Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr  
 945 950 955 960  
 Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg  
 965 970 975  
 Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro  
 980 985 990  
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
 995 1000

## (2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Trp Pro Pro Ala His Ser Gln Ala Glu Ser Arg His Gln Gln Pro Cys  
 1 5 10 15  
 His Ala Gly Leu Tyr Val Pro Gly Arg Glu Gly Arg Pro Thr Pro Arg  
 20 25 30  
 Pro Ala Pro Leu Gly Val  
 35

## (2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Gly Leu Ser Glu Cys Leu Ala Glu Ala Cys Met Ser Gly  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Arg Leu Ser Val Arg Leu Arg Pro Glu Arg Val Ser Ser Gln Gly Leu  
 1                      5                      10                      15

Ser Val Gln His Thr Cys Arg Leu His Phe Pro Thr Gly Trp Arg Ser  
                     20                      25                      30

Ala Pro Pro Gln Gly Gln Leu Phe Leu Thr Arg Ser Pro Ala Ser Thr  
                     35                      40                      45

Pro His Ile Gly Ile Val His Pro Gln Ile Arg His Cys Ser Pro Leu  
                     50                      55                      60

Ala Leu Pro Ser Phe Ala Phe His Pro His His Pro Gly Gly Asp Pro  
                     65                      70                      75                      80

Glu Lys Asp Pro Gly Ser Ser Gly Asn Leu Glu  
                     85                      90

## (2) INFORMATION FOR SEQ ID NO:340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Pro Lys Val Cys Pro Val His Arg Arg Gly Pro Cys Thr Trp Met Gly  
 1                      5                      10                      15

Val Pro Val Gly Gln Ile Gly Gly Arg Cys Cys Gly Ser Lys Ile Leu  
                     20                      25                      30

Asn Ile



## (2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Val Phe Gln Phe  
 1

## (2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Lys Lys Lys Lys Lys Lys Lys Lys  
 1 5

## (2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4037 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 56..3454  
 (D) OTHER INFORMATION: /note= "refined sequence of hTPT cDNA"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCG ATG 58  
 Met  
 1

CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC 106  
 Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His  
 5 10 15

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC<br>Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro<br>20 25 30        | 154 |
| CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG<br>Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala<br>35 40 45        | 202 |
| CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC<br>Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro<br>50 55 60 65     | 250 |
| CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG<br>Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val<br>70 75 80        | 298 |
| GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG<br>Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu<br>85 90 95        | 346 |
| GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG<br>Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu<br>100 105 110     | 394 |
| GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC<br>Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp<br>115 120 125     | 442 |
| GCA CTG CGG GGG AGC GGG GCG TGG GGG CTG CTG CTG CGC CGC GTG GGC<br>Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly<br>130 135 140 145 | 490 |
| GAC GAC GTG CTG GTT CAC CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG<br>Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu<br>150 155 160     | 538 |
| GTG GCT CCC AGC TGC GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG<br>Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln<br>165 170 175     | 586 |
| CTC GGC GCT GCC ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC<br>Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro<br>180 185 190     | 634 |
| CGA AGG CGT CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG<br>Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu<br>195 200 205     | 682 |
| GCC GGG GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG<br>Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly<br>210 215 220 225 | 730 |
| GGC AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC<br>Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly<br>230 235 240     | 778 |
| GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG GCC<br>Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala<br>245 250 255     | 826 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CAC | CCG | GGC | AGG | ACG | CGT | GGA | CCG | AGT | GAC | CGT | GGT | TTC | TGT | GTG | GTG | 874  |
| His | Pro | Gly | Arg | Thr | Arg | Gly | Pro | Ser | Asp | Arg | Gly | Phe | Cys | Val | Val |      |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |      |
| TCA | CCT | GCC | AGA | CCC | GCC | GAA | GAA | GCC | ACC | TCT | TTG | GAG | GGT | GCG | CTC | 922  |
| Ser | Pro | Ala | Arg | Pro | Ala | Glu | Glu | Ala | Thr | Ser | Leu | Glu | Gly | Ala | Leu |      |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |      |
| TCT | GGC | ACG | CGC | CAC | TCC | CAC | CCA | TCC | GTG | GGC | CGC | CAG | CAC | CAC | GCG | 970  |
| Ser | Gly | Thr | Arg | His | Ser | His | Pro | Ser | Val | Gly | Arg | Gln | His | His | Ala |      |
| 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     | 305 |      |
| GGC | CCC | CCA | TCC | ACA | TCG | CGG | CCA | CCA | CGT | CCC | TGG | GAC | ACG | CCT | TGT | 1018 |
| Gly | Pro | Pro | Ser | Thr | Ser | Arg | Pro | Pro | Arg | Pro | Trp | Asp | Thr | Pro | Cys |      |
|     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |      |
| CCC | CCG | GTG | TAC | GCC | GAG | ACC | AAG | CAC | TTC | CTC | TAC | TCC | TCA | GGC | GAC | 1066 |
| Pro | Pro | Val | Tyr | Ala | Glu | Thr | Lys | His | Phe | Leu | Tyr | Ser | Ser | Gly | Asp |      |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |      |
| AAG | GAG | CAG | CTG | CGG | CCC | TCC | TTC | CTA | CTC | AGC | TCT | CTG | AGG | CCC | AGC | 1114 |
| Lys | Glu | Gln | Leu | Arg | Pro | Ser | Phe | Leu | Leu | Ser | Ser | Leu | Arg | Pro | Ser |      |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |      |
| CTG | ACT | GGC | GCT | CGG | AGG | CTC | GTG | GAG | ACC | ATC | TTT | CTG | GGT | TCC | AGG | 1162 |
| Leu | Thr | Gly | Ala | Arg | Arg | Leu | Val | Glu | Thr | Ile | Phe | Leu | Gly | Ser | Arg |      |
|     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |      |
| CCC | TGG | ATG | CCA | GGG | ACT | CCC | CGC | AGG | TTG | CCC | CGC | CTG | CCC | CAG | CGC | 1210 |
| Pro | Trp | Met | Pro | Gly | Thr | Pro | Arg | Arg | Leu | Pro | Arg | Leu | Pro | Gln | Arg |      |
| 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     | 385 |      |
| TAC | TGG | CAA | ATG | CGG | CCC | CTG | TTT | CTG | GAG | CTG | CTT | GGG | AAC | CAC | GCG | 1258 |
| Tyr | Trp | Gln | Met | Arg | Pro | Leu | Phe | Leu | Glu | Leu | Leu | Gly | Asn | His | Ala |      |
|     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |     |      |
| CAG | TGC | CCC | TAC | GGG | GTG | CTC | CTC | AAG | ACG | CAC | TGC | CCG | CTG | CGA | GCT | 1306 |
| Gln | Cys | Pro | Tyr | Gly | Val | Leu | Leu | Lys | Thr | His | Cys | Pro | Leu | Arg | Ala |      |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |      |
| GGC | GTC | ACC | CCA | GCA | GCC | GGT | GTG | TGT | GCC | CGG | GAG | AAG | CCC | CAG | GGC | 1354 |
| Ala | Val | Thr | Pro | Ala | Ala | Gly | Val | Cys | Ala | Arg | Glu | Lys | Pro | Gln | Gly |      |
|     |     | 420 |     |     |     | 425 |     |     |     |     |     | 430 |     |     |     |      |
| TCT | GTG | GCG | GCC | CCC | GAG | GAG | GAG | GAC | ACA | GAC | CCC | CGT | CGC | CTG | GTG | 1402 |
| Ser | Val | Ala | Ala | Pro | Glu | Glu | Glu | Asp | Thr | Asp | Pro | Arg | Arg | Leu | Val |      |
|     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     |      |
| CAG | CTG | CTC | CGC | CAG | CAC | AGC | AGC | CCC | TGG | CAG | GTG | TAC | GGC | TTC | GTG | 1450 |
| Gln | Leu | Leu | Arg | Gln | His | Ser | Ser | Pro | Trp | Gln | Val | Tyr | Gly | Phe | Val |      |
| 450 |     |     |     |     | 455 |     |     |     | 460 |     |     |     |     |     | 465 |      |
| CGG | GCC | TGC | CTG | CGC | CGG | CTG | GTG | CCC | CCA | GGC | CTC | TGG | GGC | TCC | AGG | 1498 |
| Arg | Ala | Cys | Leu | Arg | Arg | Leu | Val | Pro | Pro | Gly | Leu | Trp | Gly | Ser | Arg |      |
|     |     |     |     | 470 |     |     |     | 475 |     |     |     |     |     | 480 |     |      |
| CAC | AAC | GAA | CGC | CGC | TTC | CTC | AGG | AAC | ACC | AAG | AAG | TTC | ATC | TCC | CTG | 1546 |
| His | Asn | Glu | Arg | Arg | Phe | Leu | Arg | Asn | Thr | Lys | Lys | Phe | Ile | Ser | Leu |      |
|     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |     |      |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG ATG AGC<br>Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser<br>500 505 510     | 1594 |
| GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT GGC TGT GTT<br>Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val<br>515 520 525     | 1642 |
| CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG GCC AAG TTC CTG<br>Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu<br>530 535 540 545 | 1690 |
| CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG CTC AGG TCT TTC TTT<br>His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe<br>550 555 560     | 1738 |
| TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG CTC TTT TTC TAC CGG<br>Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg<br>565 570 575     | 1786 |
| CCG AGT GTC TGG AGC AAG TTG CAA AGC ATT GGA ATC AGA CAG CAC TTG<br>Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu<br>580 585 590     | 1834 |
| ARG AGG GTG CAG CTG CGG GAG CTG TCG GAA GCA GAG GTC AGG CAG CAT<br>Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His<br>595 600 605     | 1882 |
| CGG GAA GCC AGG CCC GCC CTG CTG ACG TCC AGA CTC CGC TTC ATC CCC<br>Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro<br>610 615 620 625 | 1930 |
| AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA<br>Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly<br>630 635 640     | 1978 |
| GTC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG<br>Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg<br>645 650 655     | 2026 |
| GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC<br>Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro<br>660 665 670     | 2074 |
| GCC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC<br>Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala<br>675 680 685     | 2122 |
| TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG<br>Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu<br>690 695 700 705 | 2170 |
| CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC<br>Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro<br>710 715 720     | 2218 |
| CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC<br>Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn<br>725 730 735     | 2266 |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG<br>Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly<br>740 745 750     | 2314 |
| CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC<br>His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu<br>755 760 765     | 2362 |
| CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG<br>Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro<br>770 775 780 785 | 2410 |
| CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC<br>Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala<br>790 795 800     | 2458 |
| AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC<br>Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala<br>805 810 815     | 2506 |
| GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG<br>Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln<br>820 825 830     | 2554 |
| GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG<br>Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser-Leu Cys Tyr Gly Asp Met<br>835 840 845     | 2602 |
| GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT<br>Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg<br>850 855 860 865 | 2650 |
| TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA<br>Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys<br>870 875 880     | 2698 |
| ACC TTC CTC AGG ACC CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG<br>Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val<br>885 890 895     | 2746 |
| GTG AAC TTG CGG AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC<br>Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala<br>900 905 910     | 2794 |
| CTG GGT GGC ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC<br>Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro<br>915 920 925     | 2842 |
| TGG TGC GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC<br>Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp<br>930 935 940 945 | 2890 |
| TAC TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC<br>Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe Asn<br>950 955 960     | 2938 |
| CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC<br>Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val<br>965 970 975     | 2986 |

|                                                                                                                                                           |      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC<br>Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser<br>980 985 990         | 3034 |
| CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG GCG<br>Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala<br>995 1000 1005       | 3082 |
| TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG CAA GTT<br>Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val<br>1010 1015 1020 1025 | 3130 |
| TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC TCT GAC ACG GCC TCC<br>Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser<br>1030 1035 1040      | 3178 |
| CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC GCA GGG ATG TCG CTG GGG<br>Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly<br>1045 1050 1055      | 3226 |
| GCC AAG GGC GCC GCC GGC CCT CTG CCC TCC GAG GCC GTG CAG TGG CTG<br>Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu<br>1060 1065 1070      | 3274 |
| TTC CAC CAA GCA TTC CTG CTC AAG CTG ACT CGA CAC CGT GTC ACC TAC<br>Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr<br>1075 1080 1085      | 3322 |
| CTG CCA CTC CTG GGG TCA CTC AGG ACA GCC CAG ACG CAG CTG AGT CGG<br>Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg<br>1090 1095 1100 1105 | 3370 |
| AAG CTC CCG GGG ACG ACG CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG<br>Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro<br>1110 1115 1120      | 3418 |
| TCA CTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CCGCCACAG<br>Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp<br>1125 1130                              | 3471 |
| CCAGGCGGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA                                                                                         | 3531 |
| GGGGCGGGCC ACACCCAGGC CCGCACCGCT GGGAGTCTGA GGCCTGAGTG AGTGTTCGGC                                                                                         | 3591 |
| CGAGGCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCCAG                                                                                         | 3651 |
| CCAAGGGCTG AGTGTCCAGC ACACCTGCCG TCTTCACTTC CCCACAGGCT GGCGCTCGGC                                                                                         | 3711 |
| TCCACCCGAG GGCCAGCTTT TCYTCACCAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT                                                                                         | 3771 |
| AGTCCATCCC CAGATTGCCC ATTGTTCAAC CYTCGCCCTG CCYTCCTTTG CTTCCACCC                                                                                          | 3831 |
| CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC                                                                                         | 3891 |
| AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGGTCC CTGTGGGTCA                                                                                         | 3951 |
| AATTGGGGGG AGGTGCTGTG GGAGTAAAT ACTGAATATA TGAGTTTTTC AGTTTTGAA                                                                                           | 4011 |
| AAAAAAAAA AAAAAAAAAA AAAAAA                                                                                                                               | 4037 |

## (2) INFORMATION FOR SEQ ID NO:344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270

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Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575  
 Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
 580 585 590



Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
 595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
 625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
 645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
 660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg  
 675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
 690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile  
 705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
 725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His  
 740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp  
 755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser  
 770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu  
 785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His  
 805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro  
 820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp  
 835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu  
 850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala  
 865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys  
 885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu  
 900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe  
 915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser  
 930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe  
 945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly  
 965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn  
 980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln  
 995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln  
 1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala  
 1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu  
 1045 1050 1055

Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp  
 1060 1065 1070

Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr  
 1075 1080 1085

Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser  
 1090 1095 1100

Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn  
 1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
 1125 1130

## (2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = hydrophobic amino acid,  
 Ala, Leu, Ile, Val, Pro, Phe, Trp  
 or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Phe or Tyr"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Xaa Xaa Asp Asp Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Phe or Tyr"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Xaa Xaa Asp Asp Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Trp Xaa Gly Xaa Ser Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Xaa Leu Gly Xaa Xaa Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:349:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = hydrophobic amino acid,  
Ala, Leu, Ile, Val, Pro, Phe, Trp  
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 13  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = polar amino acid, Gly,  
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 19  
(C) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = polar amino acid, Gly,  
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 23  
(C) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = polar amino acid, Gly,  
Ser, Thr, Tyr, Cys, Asn or Gln"

(ki) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Trp Leu Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Thr  
1 5 10 15

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Arg Lys Xaa Xaa  
20 25 30

Tro

## (2) INFORMATION FOR SEQ ID NO: 350:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (11) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 2  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- ```
(A) NAME/KEY: Modified-site
(3) LOCATION: 7..8
(D) OTHER INFORMATION: /product= "OTHER"
                        /note= "Xaa = hydrophobic amino acid,
                        Ala, Leu, Ile, Val, Pro, Phe, Trp
                        or Met"
```

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 10..11
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 13
(C) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 21
(C) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 25
(C) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(IX) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 28..29
(D) OTHER INFORMATION: /product= "OTHER" -
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 31
(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1 5 10 15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
20 25 30

Xaa Trp

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7..8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10..11
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe, Trp
or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Gln or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = polar amino acid, Gly,
Ser, Thr, Tyr, Cys, Asn or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29..30
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Lys or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1          5          10          15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
          20          25          30

Xaa Xaa Trp
          35

```

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) -SEQUENCE DESCRIPTION: SEQ ID NO:352:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1          5          10          15

Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa
          20          25          30

Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
          35          40

```

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```

Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr
1           5           10           15
Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa
20           25           30
Xaa Xaa Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
35           40

```

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

```

Glu Xaa Xaa Val Xaa
1           5

```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

```

Xaa Xaa Xaa Arg Xaa Xaa Pro Lys Xaa Xaa Xaa
1           5           10

```

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

```

Xaa Arg Xaa Ile Xaa
1           5

```

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Tyr Asp Xaa
 1 5 10 15
 Xaa

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Tyr Xaa Xaa Xaa Xaa Gly Xaa Xaa Gln Gly Xaa Xaa Xaa Ser Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa
 20

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Xaa Xaa Xaa Xaa Xaa Xaa Asp Asp Xaa Leu Xaa Xaa Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Phe Phe Tyr Xaa Thr Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Phe Phe Tyr Val Thr Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

TTYTTYTAYG TNACNGA

17

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

TCNGTNACRT ARAARAA

17

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Arg Phe Ile Pro Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

MMNTTATAC CAAACCC

17

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GGYTTNGGDA TRAANC

16

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Ala Tyr Asp Thr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GCNTAYGAYA CNAT

14

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

TANGTRTCRT ANG

14

(2) INFORMATION FOR SEQ ID NO:370:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Gly Ile Pro Gln Gly
1 5

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GGNATHCCNC ARGG

14

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

SWNCCYTGNG GDATNCC

17

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Leu Val Asp Asp Phe Leu
1 5

(2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

YTNGTNGAYG AYTTYT

17

(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Asp Asp Phe Leu Leu Val Thr
1 5

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GTACACARNA RRAARTCTC

20

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCPl.1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GTGAAGGCAC TGTTGACG

19

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.15 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

CGCGTGGGTG AGGTGAGGTG

20

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.14 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

CTGTGCTGGG CCTGGACGAT A

21

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "billTCP6 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

AGCTTGGTCT CCATGTCGCC GTAG

24

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GTGGATGATT TCTTGTTGG

19

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.6 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.7 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.8 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

CAGCAGGAGG ATCTTGTAG

19

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.9 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

TGACCCGAGG AGTGGCAGG

19

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.10 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

TCAAGCTGAC TCGACACCG

19

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "TCPl.11 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

CGGCGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCPl.12 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GCTGAAGGCT GAGTGTCC

18

(2) INFORMATION FOR SEQ ID NO:391:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.13 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.16 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

TTTCCGTGTT GAGTGTTC

19

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.17 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GTCACCGTGT TGGGCAGG

18

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.19 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GCTACCTGCC CAACACGG

18

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCP1.20 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GCGCGAAGAA CGTGCTGG

18

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.21 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

CACTGCTCCT TGTCGCCTG

19

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.22 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

TTCCCAAGGA CTTTGTTC

19

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.24 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

TGTTCTCAA GACGCACTG

19

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.25 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

TACTGCGTGC GTCGGTATG

19

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.26 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GCTCTTGCGG CTGAAGTGT

19

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.27 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

TGGTTCACCT GCTGGCACG

19

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.28 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GTGGTTTCTG TGTGGTGTG

19

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.29 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GACACACAC AGAAACCAC

19

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.30 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GTGCCAGCAG GTGAACCAG

19

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.32B primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GCAGTGGCGTC TTGAGGAGC

19

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.33 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

TGGAACCATA GCGTCAGGGA G

21

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.34 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GGCCTCCCTG ACGCTATGGT T

21

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.35 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

GCKCGGCGCT GCCACTCAGG

20

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.35t primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GCTCGGCGCT GCCACTCAGG

20

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.36 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

ACGCCGAGAC CAAGCACTTC

20

(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.38 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

CCAAAGAGGT GGCTTCTTCG

20

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.39 primer"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.42 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

.GGCGACGACG TGCTGGTTC

19

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.43 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GGCTCAGGGG CAGCGCCAC

19

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.44 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

CTGGCAGGTG TACGGCTTC

19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

AAGGCCAGCA CGTTCTTCGC

20

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.40 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

CACGTTTCGTG CGGCGCCTG

19

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.41 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

CCTTCACCAC CAGCGTGCG

19

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.45 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

GCGTGGACCG AGTGACCGTG GTTTC

25

(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.46 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GACGTGGTGG CCGCGATGTG G

21

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TCP1.47 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GAAGTCTGCC GTTGCCCAAG AG

22

(2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.48 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GACACCACAC AGAAACCACG GTCAC

25

(2) INFORMATION FOR SEQ ID NO:422:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.49 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

CGCCCCCTCC TTCCGCCAGG T

21

(2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.50 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

CGAAGCCGAA GGCCAGCACG TTCTT

25

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TCP1.51 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GGTGGCCCGA GTGCTGCAGA GG

22

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.52 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GTAGCTGCGC ACGCTGGTGG TGAAG

25

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TCP1.53 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

TGGGCGACGA CGTGCTGGTT CA

22

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note="TCP1.54 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

TATGGTTCCA GGCCCGTTTCG CATCC

25

(2) INFORMATION FOR SEQ ID NO:428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TCP1.55 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

CCAGCTGCGC CTACCAGGTG TGC

23

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCPl.56 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

GGCCTCCCTG ACGCTATGGT TCCAG

25

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TCPl.57 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GGTGCTGCCG CTGGCCACGT TCG

23

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.58 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

TCCCAGGGCA CGCACACCAG GCACT

25

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.59 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GTACAGGGCA CACCTTTGGT CACTC

25

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.60 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

TCGACGACGT ACACACTCAT CAGCC

25

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.61 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

AGCGGCAGCA CCTCGCGGTA GTGGC

25

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.62 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

CCACCAGCTC CTTCAGGCAG GACAC

25

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.63 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

CCAGGGCTTC CCACGTGCGC AGCAG

25

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.64 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

CGCACGAACG TGGCCAGCGG CAGCA

25

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TCP1.65 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

TGACCGTGGT TTCTGTGTGG TGT

23

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.66 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

CCCTCTTCAA GTGCTGTCTG ATTCC

25

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.67 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

ATCGCGGCCA CCACGTCCCT

20

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.68 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

TGCTCCAGAC ACTCGGCCGG TAGAA

25

(2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.69 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

ACGAAGCCGT ACACCTGCC

19

(2) INFORMATION FOR SEQ ID NO:443:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP1.72 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

CGACATCCCT GCGTTCTTGG CTTTC

25

(2) INFORMATION FOR SEQ ID NO:444:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.73 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

CACTGCTGGC CTCATTCAGG G

21

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TCPl.74 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GCGACATGGA GAACAAGC

18

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCPl.75 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GCAGCCATAC TCAGGGACAC

20

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "TCP1.76 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

CCATCCTCTC CACGCTGCTC

20

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TCP1.77 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GCGATGACCT CCGTGAGCCT G

21

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.78 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

CCCAGGACAG GCTCACGGA

19

2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "billTCP1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

CCTCTTCAAG TGCTGTCTGA TTCC

24

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "billTCP2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

CAGCTCGACG ACGTACACAC TCATC

25

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "billTCP4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

CTGACGTCCA GACTCCGCTT CAT

23

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: /note= "rpprim01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GACCTGAGCA GCTCGACGAC GTACACACTC ATC

33

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Ltl primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GTCGTCGAGC TGCTCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

AGCACGCTGA ACAGTGCCTT

20

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GACCTGAGCA GCTCGACGAC

20

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

AAGGCACTGT TCAGCGTGCT

20

(2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Lt5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

CGGCCGAGTG TCTGGAGCAA

20

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "Lt6 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GGATGAAGCG GAGTCTGGA

19

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "BamH1Lt7 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

ATGGATCCGT CGTCGAGCTG CTCAGGTCT

29

(2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "Sal1Lt8 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

ATCAGCTGAG CACGCTGAAC AGTGCCTTC

29

(2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "K303 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GTCTCCGTGA CATAAAAGAA AGAC

24

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "K304 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

GCCAAGTTCC TGCCTGGCT

20

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "K305 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GCCTGTTCTT TTGAAACGTG GTCT

24

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "K306 primer"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = guanosine substituted by two
biotin groups"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

NCCTGTTCTT TTGAAACGTG GTCT

24

(2) INFORMATION FOR SEQ ID NO:466:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "K311 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GTCAAGATGC CTGAGATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "K312 and K313 primers"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

TGCTTAGCTT GTGGGGGTGT CA

22

(2) INFORMATION FOR SEQ ID NO:468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "K320 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GCTGCGTCCT GCTGCGCACG T

21

(2) INFORMATION FOR SEQ ID NO:469:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "K321 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

CAGCGGGGAG CGCGCGGCAT C

21

(2) INFORMATION FOR SEQ ID NO:470:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "K322 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

TGGGCCACCA GCGCGCGGAA A

21

(2) INFORMATION FOR SEQ ID NO:471:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "slanti.1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

CGGCCGCAGC CCGTCAGGCT TGGGG

25

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /note= "slanti.2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

CCGACAGCTC CCGCAGCTGC ACCC

24

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "slanti.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

CGTACACACT CATCAGCCAG TGCAGGA ACT TGGC

34

(2) INFORMATION FOR SEQ ID NO:474:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /note= "slanti.4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

CGCGCCCGCT CGTAGTTGAG CACGCTGAAC AGTGCCTTCA CCCTCG

46

(2) INFORMATION FOR SEQ ID NO:475:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "slanti.5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GGCGAGTCTG GACGTCAGCA GGGCGGGCCT GGCTTCCCG

39

(2) INFORMATION FOR SEQ ID NO:476:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "UTR2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

ATTTGACCCA CAGGGACCCC CATCCAG

27

(2) INFORMATION FOR SEQ ID NO:477:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "FW5 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

ATGACCGCCC TCCTCGTGAG

20

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GCCACCCCCG CGATGCC

17

(2) INFORMATION FOR SEQ ID NO:479:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

AGCCCTGGCC CCGGCCA

17

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

TCCCACGTGC GCAGCAG

17

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Nam4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

AGCAGGACGC AGCGCTG

17

(2) INFORMATION FOR SEQ ID NO:482:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "PE01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

CGCGGTAGTG GCTGCGCAGC AGGGAGCGCA CGGC

34

(2) INFORMATION FOR SEQ ID NO:483:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "PE02 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

CCAGGGGOTTC CCACGTGCCG AGCAGGACGC AGCGC

35

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: /note= "LM101 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

CTAGTCTAGA TCRCTAGCGT AATCTGGAAC ATCGTATGGG TRTCCAGGAT GGTCTTGAAG

60

TC

62

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "LM103 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

TACCATGGGC TACCCATACG ACGTTCCAGA TTACGCTCA

39

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "LM104 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

TATGAGCGTA ATCTGGAACG TCGTATGGGT AGCCCATGG

39

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: /note= "LM105 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GTGTACGTCG TCGAGCTCCT CAGGTCTGCC TTTTATGTCA CGGAG

45

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "LM106 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

GTGTACGTCG TCGAGCTCCT CAGGTCTTTC GCTTATGTCA CGGAGACC

48

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "LM107 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

CCTCAGGTCT TTCTTTGCTG TCACGGAGAC AACGTTTCAA AAGAACAG

48

(2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /note= "LM108 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

GGTCTTTCTT TTATGTCGCG GAGACAACGT TTCAAAGAA CAG

43

(2) INFORMATION FOR SEQ ID NO:491:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: /note= "LM109 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

CTTCTTTTGA TGTCACGGCG ACAACGTTTC AAAAGAACAG

40

(2) INFORMATION FOR SEQ ID NO:492:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: /note= "LM_FFYTE primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

ATGAGTGTGT ACGTCGTCGA GTCCTCAGG TCTACCACGT TTCAAAAGAA CAGGCTCTTT 60
TTC 63

(2) INFORMATION FOR SEQ ID NO:493:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "TCP061 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GGCTGATGAG TGTGTACGTC GTCGA - 25

(2) INFORMATION FOR SEQ ID NO:494:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "HUM01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

ACGTGGTCTC CGTGACATAA AAGAA 25

(2) INFORMATION FOR SEQ ID NO:495:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "HUMO2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

AGGTCTTTCT TTTATGTCAC GGA

23

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "HUMO3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

CACAGACCCC CGTCGCCTGG TC

22

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "HUMO4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

CGGAGTCTGG ACGTCAGCAG GGC

23

(2) INFORMATION FOR SEQ ID NO:498:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F1N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

CGCGGATCCG TAACTAAAT GCCGCGCGCT CCCCCTGCTGC

39

(2) INFORMATION FOR SEQ ID NO:499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F1C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

CCGGAATTCG TTAGTTACTT ACAAAGAGGT GGCTTCTTCG GC

42

(2) INFORMATION FOR SEQ ID NO:500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F2N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

CGCGGATCCG TAACTAAAGC CACCTCTTTG GAGGGTGCG

39

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F2C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

CCGGAATTCG TTAGTTACTT AAGACCTGAG CAGCTCGACG AC

42

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F3N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

CGCGGATCCG TAACTAAAAT GAGTGTGTAC GTCGTCGAG

39

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F3C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

CCGGAATTCG TTAGTTACTT AGATCCCCTG GCACTGGACG

40

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /note= "SLW F4N primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

CGCGGATCCG TAACTAAAAT CCCGCAGGGC TCCATCCTC

39

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: /note= "SLW F4C primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

CCGGAATTCG TTAGTTACTT AGTCCAGGAT GGTCTTGAAG TC

42

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "40-60 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GGCATCGCGG GGGTGGCCGG G

21

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "260-280 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GGACACCTGG CGGAAGGAGG G

21

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "500-520 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GCGTGCCAGC AGGTGAACCA G

21

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "770-790 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

CTCAGGGGCA GCGCCAGGCC T

21

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "885-905 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

AGGTGGCTTC TTCGGCGGGT C

21

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "1000-1020 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GGACAAGGCG TGTCCCAGGG A

21

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "1300-1320 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

GCTGGGGTGA CCGCAGCTCG C

21

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "1520-1540 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GATGAACTTC TTGGTGTTC T

21

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2110-2130 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GTGCGCCAGG CCCTGTGGAT A

21

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2295-2315 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GCCCCATGGGC GGCCTTCTGG A

21

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2450-2470 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GAGGCCACTG CTGGCCTCAT T

21

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "2670-2690 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GGGTGAGGTG AGGTGTCACC A

21

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "3080-3110 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GCTGCAGCAC ACATGCGTGA AACCTGTACG C

31

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "3140-3160 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GACGCGCAGG AAAAATGTGG G

21

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "3690-3710 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

CCGAGCGCCA GCCTGTGGGG A

21

(2) INFORMATION FOR SEQ ID NO:521:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "55-75 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

CAGCGGGGAG CGCGCGGCAT C

21

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "phosphorothioate"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "151-171 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

CAGCACCTCG CGGTAGTGGC T

21

(2) INFORMATION FOR SEQ ID NO:523:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TP1.1 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

TCAAGCCAAA CCTGAATCTG AG

22

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "TPl.2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

CCCGAGTGAA TCTTTCTACG C

21

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "TPl.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GTCTCTGGCA GTTTCCTCAT CCC

23

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "TP1.4 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

TTTAGGCATC CTCCCAAGCA CA

22

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

TTAGGGTTAG

10

(2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

TTAGGGTTAG GGTAGGG

18

(2) INFORMATION FOR SEQ ID NO:529:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GTTAGGGTTA GGGTTAGG

18

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "sequence (CCCTAA)-n, where n is at least 1, or at least 3, or at least 10 or more"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

CCCTAACCCCT AACCCCTAACC CTAACCCTAA CCCTAACCCCT AACCCCTAACC CTAACCCTAA 60

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN TTAG 34

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN AGGG

34

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN TTAGGGTTAG

40

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN TTAGGGTTAG GGTTAG

46

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAGGGTTAG GGTTAGGGTT AG

52

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "non-telomeric nucleotide sequence, (X)-n, where n is 8-20, or 6-30"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTAGGGTTAG GGTTAGGGTT AGGGTTAG

58

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..10
- (D) OTHER INFORMATION: /note= "primer terminating at template boundary"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

TAGGGATTAG

10

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /note= "primer for hTERT nucleolytic assay"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 3'-deoxyguanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

TTAGGGTTAG GGTAN

16

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: repeat_unit
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "sequence (TTAGGG)-n, where n is 1-10, or typically 3-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

TTAGGGTTAG GGTTAGGGTT AGGGTTAGGG TTAGGGTTAG GGTTAGGGTT AGGGTTAGGG

60

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Trp Xaa Gly Xaa Ser
1 5

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

Pro Arg Arg Arg
1

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

Pro Lys Arg Pro Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:543:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "antisense hTRT molecule"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GCTCTAGAAT GAAGGGTG

18

(2) INFORMATION FOR SEQ ID NO:544:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "S1 control oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GCGACGACTG ACATTGGCCG G

21

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "S2 control oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GGCTCGAAGT AGCACCGGTG C

21

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "S3 control oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GTGGGAACAG GCCGATGTCC C

21

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ON1 oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

TCCCACGTGC GCAGCAGGAC GCAGCGCTGC

30

(2) INFORMATION FOR SEQ ID NO:548:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ON2 oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GCCGGGGCCA GGGCTTCCCA CGTGCGCAGC

30

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ON3 oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GGCATCGCGG GGGTGGCCGG GGCCAGGGCT

30

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "delta-182 species specific primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

GGCACTGGAC GTAGGACGTG

20

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "293 cell line lambda cDNA library PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

CGGAAGAGTG TCTGGAGCAA

20

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "GAPDH control primer K136"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

CTCAGACACC ATGGGGAAGG TGA

23

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "GAPDH control primer K137"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

ATGATCTTGA GGCTGTTGTC ATA

23

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "competitor oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

TAGACCTGTT AGTGACATT TGAATTGAAG C

31

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "competitor oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "biotin-labeled
telomerase-specific oligonucleotide"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = thymidine modified by a
biotin group"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 12..13
- (D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 14..17
- (D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18..21
- (D) OTHER INFORMATION: /mod_base= gm

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 22..25
- (D) OTHER INFORMATION: /mod_base= um

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /mod_base= gm

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

UAGACCTGTT AMNNNNNNNNNN NNNNNN

26

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "displacement
deoxyoligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

CAAAACCCCA AAACCTAACA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:558:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: /note= "5' primer encoding a hammerhead ribozyme, a T7-promoter and an EcoRI site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GGGGGAATTC TAATACGACT CACTATAGGG AAGAACTCT GATGAGGCCG AAAGGCCGAA

60

ACTCCACGAA AGTGGAGTAA GTTCTCGAT AATTGATCTG TAG

103

(2) INFORMATION FOR SEQ ID NO:559:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "3' primer including an EarI site and a BamHI site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

CGGGGATCCT CTTCAAAGA TGAGAGGACA GCAAAC

36

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

CCCCAAAACC CCAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTGGG GGTTTGGGG 60

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

CCAAAACCCC AAAACCCCAA AACCCCCACA GGGGTTTGGG GGTTTGGGG TTTTGGGG 58

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

AAAACCCCAA AACCCCAAAA CCCCCACAGG GGGTTTGGGG TTTTGGGGTT TTGGGG 56

(2) INFORMATION FOR SEQ ID NO:563:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..54
(D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT GGGG

54

(2) INFORMATION FOR SEQ ID NO:564:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..43
(D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

CCCAAAACC CCAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:565:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..52
(D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

AAAACCCCAA AACCCCAAAA CCCCACAGG GGTTTTGGGG TTTGGGGTT TT

52

(2) INFORMATION FOR SEQ ID NO:566:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTGGGGTT TTGGGGTTTT

50

(2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

CCAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTTGG GGTTTT

46

(2) INFORMATION FOR SEQ ID NO:568:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..44
- (D) OTHER INFORMATION: /note= "hairpin primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

AAAACCCCAA AACCCCCACA GGGGTTTTGG GGTTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Euplotes telomerase 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

TCTRAARTAR TGDGTNAORT TRTTCAT

27

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Euplotes telomerase 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GCGGATCCAT GAAYCCWGAR AAYCCWAAYG T

31

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide
primer for cloning of Euplotes
telomerase 43 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

NNNGTNACHG GHATHAAYAA

20

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide
primer for cloning of Euplotes
telomerase 43 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

GGCDGTYTCY TGRTCRTTTRT A

21

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Oxytricha trifallax telomerase homologous to Euplotes 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "degenerate oligonucleotide primer for cloning of Oxytricha trifallax telomerase homologous to Euplotes 123 kDa protein subunit"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

DGTGATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K231 forward primer"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = guanosine modified by a
biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

NCCTATTTT TYTAYNNNAC NGA

23

(2) INFORMATION FOR SEQ ID NO:576:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K220 reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:577:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

Asp Asp Phe Leu Xaa Ile
1 5

(2) INFORMATION FOR SEQ ID NO:578:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K228 forward primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

ACAATGGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:579:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2..3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Arg Xaa Xaa Pro Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:580:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "K224 reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

ACGAATCKNG GDATNSWRTC RTARCA

26

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

Cys Tyr Asp Ser Ile Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:582:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "K227 reverse primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Asp Ile Lys Ser Cys Tyr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: /note= "clone 168-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

```

GATTACTCCC GAAGAAAGGA TCTTCCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC      60
AAAAAATAT TAAGTTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACTT GTGTTTAGGA      120
ATTTAAAAGA CATGCTGGGA TAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATTT      180
CAGAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAAATAA AGGAAGACCT CAGCTATATT      240
ATGTCACTCT AGACATAAAG ACTTGCTAC                                     269

```

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "K297 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

```

GAGTGACATA ATATACGTGA                                             20

```

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: /note= "Tetrahymena DNA fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

```

AAACACAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT      60
AAATTAACTA TTGTCAAAGT AAGAATTTAG TTTTCTGAAA AGAATAAATA AATGAAAAAT      120
AATTTTTATC AAAAAATTTA GCTTGAAGAG GAGAATTTGG AAAAAAGTTGA AGAAAAATTG      180
ATACCAGAAG ATTCATTTTA GAAATACCCT CAAGGAAAGC TAAGGATTAT ACCTAAAAAA      240
GGATCTTTCC GTCCAATCAT GACTTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA      300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTTA GGAATTTAAA AGACATGCTG      360
GGATAAAGA TAGGATACTC AGTCTTTGAT AATAAACAAA TTTCAGAAAA ATTTGCCTAA      420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA          474

```

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /note= "Q-T primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

```

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTTT TTTTTTTTTT      50

```

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Q-O primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

CCAGTGAGCA GAGTGACG

18

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "M2-T primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GTGTCATTTTC TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Q-I primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAGGACTCGA GCTCAAGC

18

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "M2-T2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

ACCTATCGTT TACGAAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "M2-B primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

CACTGATCCT TTCTTTTTCG TAAACGATAG GT

32

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /note= "M2-B2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

CATCAATCAA ATCTTCATA TAGAAATGAC A

31

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "PCR Adapt SfiI primer"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = 5'-phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

NGGCCGTGTT GGCCTAGTTC TCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: /note= "PCR Adapt SfiII primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCCCC

38

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "TCP1.3 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "F3b primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

TCTAACCCCTA ACTGAGAAGG GCGTAG

26

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "R3c primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

GTTTGCTCTA GAATGAACGG TGGAAG

26

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: /note= "104-base intronic sequence (SEQ ID NO:7) inserted at the junction corresponding to bases 274 and 275 of hTRT (SEQ ID NO:1)"

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 28..131
- (D) OTHER INFORMATION: /note= "intronic sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

CCCCCGCCG CCCCTCCTT CCGCCAGGTG GGCCTCCCG GGGTCGGCGT CCGGCTGGGG 60

TTGAGGGCGG CCGGGGGGAA CCAGCGACAT GCGGAGAGCA GCGCAGGCGA CTCAGGGCGC 120

TTCCCCCGCA GGTGTCCTGC CTGAAGGAGC TGGTGGCCCG AGTGCTGCAG 170

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1285
- (D) OTHER INFORMATION: /note= "fusion protein composed of enterokinase cleavable, His tagged thioredoxin moiety and full length hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Met	Ser	Asp	Lys	Ile	Ile	His	Leu	Thr	Asp	Asp	Ser	Phe	Asp	Thr	Asp		
1				5					10					15			
Val	Leu	Lys	Ala	Asp	Gly	Ala	Ile	Leu	Val	Asp	Phe	Trp	Ala	His	Trp		
			20					25					30				
Cys	Gly	Pro	Cys	Lys	Met	Ile	Ala	Pro	Ile	Leu	Asp	Glu	Ile	Ala	Asp		
		35					40					45					
Glu	Tyr	Gln	Gly	Lys	Leu	Thr	Val	Ala	Lys	Leu	Arg	Ile	Asp	His	Asn		
	50					55					60						
Pro	Gly	Thr	Ala	Pro	Lys	Tyr	Gly	Ile	Arg	Gly	Ile	Pro	Thr	Leu	Leu		
65					70					75				80			
Leu	Phe	Lys	Asn	Gly	Glu	Val	Ala	Ala	Thr	Lys	Val	Gly	Ala	Leu	Ser		
			85						90					95			
Lys	Gly	Gln	Leu	Lys	Glu	Phe	Leu	Asp	Ala	Asn	Leu	Ala	Gly	Ser	Gly		
			100					105					110				
Ser	Gly	Asp	Asp	Asp	Asp	Lys	Val	Pro	Met	His	Glu	Leu	Glu	Ile	Phe		
		115					120					125					
Glu	Phe	Ala	Ala	Ala	Ser	Thr	Gln	Arg	Cys	Val	Leu	Leu	Arg	Thr	Trp		
	130					135					140						
Glu	Ala	Leu	Ala	Pro	Ala	Thr	Pro	Ala	Met	Pro	Arg	Ala	Pro	Arg	Cys		
145				150						155					160		
Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	His	Tyr	Arg	Glu	Val	Leu	Pro		
			165						170					175			
Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	Gln	Gly	Trp	Arg	Leu	Val		
		180						185					190				
Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala	Leu	Val	Ala	Gln	Cys	Leu		
	195						200					205					
Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro	Pro	Ala	Ala	Pro	Ser	Phe		
	210					215					220						
Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg		
225					230					235				240			
Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu		
			245					250						255			
Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val		
		260					265						270				
Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly		
		275				280						285					
Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His		
	290					295				300							
Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala		
305				310					315					320			

Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 325 330 335
 Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 340 345 350
 Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 355 360 365
 Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser
 370 375 380
 Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 385 390 395 400
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 405 410 415
 Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 420 425 430
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 435 440 445
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 450 455 460
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 465 470 475 480
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 485 490 495
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 500 505 510
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 515 520 525
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 530 535 540
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 545 550 555 560
 Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 565 570 575
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 580 585 590
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 595 600 605
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 610 615 620
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 625 630 635 640

Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 645 650 655
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 660 665 670
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 675 680 685
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 690 695 700
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 705 710 715 720
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 725 730 735
 Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 740 745 750
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 755 760 765
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 770 775 780
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 785 790 795 800
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 805 810 815
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 820 825 830
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 835 840 845
 Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val
 850 855 860
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 865 870 875 880
 Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 885 890 895
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 900 905 910
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 915 920 925
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 930 935 940
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 945 950 955 960

Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 965 970 975
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 980 985 990
 Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 995 1000 1005
 Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
 1010 1015 1020
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 1025 1030 1035 1040
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 1045 1050 1055
 Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 1060 1065 1070
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 1075 1080 1085
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 1090 1095 1100
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1105 1110 1115 1120
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1125 1130 1135
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1140 1145 1150
 Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1155 1160 1165
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1170 1175 1180
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1185 1190 1195 1200
 Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly
 1205 1210 1215
 Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu
 1220 1225 1230
 Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser
 1235 1240 1245
 Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr
 1250 1255 1260
 Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe
 1265 1270 1275 1280

Lys Thr Ile Leu Asp
1285

(2) INFORMATION FOR SEQ ID NO:601:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Gly Ser Val Thr Lys
1 5

(2) INFORMATION FOR SEQ ID NO:602:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 538 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..538

(C) OTHER INFORMATION: /note= "fusion protein composed of
 glutathione-S-transferase sequence,
 thrombin cleavage sequence, recognition
 sequence for heart muscle protein
 kinase, residues introduced by cloning
 and hTERT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
1				5				10						15	
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
			20					25					30		
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
		35					40					45			
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
	50					55					60				
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65					70				75					80	

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Ile Pro Gln Gly
 225 230 235 240
 Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu
 245 250 255
 Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu
 260 265 270
 Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr
 275 280 285
 Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val
 290 295 300
 Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu
 305 310 315 320
 Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp
 325 330 335
 Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr
 340 345 350
 Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Val Thr Phe Asn Arg
 355 360 365
 Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu
 370 375 380
 Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu
 385 390 395 400

Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr
 405 410 415
 Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp
 420 425 430
 Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu
 435 440 445
 Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala
 450 455 460
 Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys
 465 470 475 480
 His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val
 485 490 495
 Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg Lys
 500 505 510
 Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro Ala
 515 520 525
 Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 530 535

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..530
- (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning, eight consecutive His residues and hTRT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val His His His His His His
 225 230 235 240
 His His Gly Ser Val Thr Lys Met Ser Val Tyr Val Val Glu Leu Leu
 245 250 255
 Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
 260 265 270
 Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 275 280 285
 Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
 290 295 300
 Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
 305 310 315 320
 Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
 325 330 335
 Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 340 345 350
 Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 355 360 365

Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp
 370 375 380

Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp
 385 390 395 400

Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 405 410 415

Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 420 425 430

Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys
 435 440 445

Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr
 450 455 460

Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln
 465 470 475 480

Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser
 485 490 495

Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met
 500 505 510

Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln
 515 520 525

Gly Ile
 530

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning and hTERT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Arg Arg Ala Ser Val Gly Ser Val Thr Lys Met Ser Val Tyr
 225 230 235 240
 Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe
 245 250 255
 Gln Lys Asn Arg Leu Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu
 260 265 270
 Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu
 275 280 285
 Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu
 290 295 300
 Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro
 305 310 315 320
 Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu
 325 330 335

Lys Arg Ala Glu Arg Leu Thr Ser Arg Lys Ala Leu Phe Ser Val Leu
 340 345 350
 Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu
 355 360 365
 Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val
 370 375 380
 Arg Ala Gln Asp Pro Pro Pro Glu Tyr Phe Val Lys Val Asp Val Thr
 385 390 395 400
 Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala
 405 410 415
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val
 420 425 430
 Val Gln Lys Ala Ala His Gly Val Arg Lys Ala Phe Lys Ser His Val
 435 440 445
 Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His
 450 455 460
 Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser
 465 470 475 480
 Ser Ser Leu Asn Glu Ala Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 485 490 495
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 500 505 510
 Gln Gly Ile
 515

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning and hTRT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro		
1				5					10					15			
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu		
			20					25					30				
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
		35					40					45					
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
	50					55					60						
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
65					70					75					80		
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
				85					90					95			
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
			100					105						110			
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
		115					120					125					
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
	130					135					140						
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
145					150					155					160		
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
				165					170						175		
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
		180						185					190				
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195					200					205					
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
	210					215					220						
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Ala	Thr	Ser	Leu		
225					230					235					240		
Glu	Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg		
				245					250					255			
Gln	His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp		
			260					265						270			
Asp	Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr		
		275					280					285					
Ser	Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser		
		290				295					300						
Leu	Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe		
305					310					315					320		

Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg
 325 330 335
 Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu
 340 345 350
 Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys
 355 360 365
 Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu
 370 375 380
 Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro
 385 390 395 400
 Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val
 405 410 415
 Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu
 420 425 430
 Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys
 435 440 445
 Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr
 450 455 460
 Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly
 465 470 475 480
 Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu
 485 490 495
 Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 500 505 510
 Arg Ser

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..517
- (D) OTHER INFORMATION: /note= "fusion protein composed of glutathione-S-transferase sequence, thrombin cleavage sequence, recognition sequence for heart muscle protein kinase, residues introduced by cloning and hTERT protein fragment"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro		
1				5					10					15			
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu		
			20					25					30				
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
		35					40					45					
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
	50					55					60						
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
65					70					75					80		
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
				85					90					95			
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
			100					105					110				
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
		115					120					125					
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
	130					135					140						
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
145					150					155					160		
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
				165					170					175			
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180					185					190				
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195					200					205					
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
	210					215					220						
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	Val	Thr	Lys	Met	Pro	Arg	Ala		
225					230					235					240		
Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Ser	His	Tyr	Arg	Glu	Val		
				245					250					255			
Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	Pro	Gln	Gly	Trp	Arg		
			260					265					270				
Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	Ala	Leu	Val	Ala	Gln		
		275					280					285					
Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	Pro	Ala	Ala	Pro	Ser		
	290					295					300						
Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg	Val	Leu	Gln		
305					310					315					320		

Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala
 325 330 335
 Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Thr Thr Ser Val
 340 345 350
 Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
 355 360 365
 Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 370 375 380
 Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Cys Ala Tyr
 385 390 395 400
 Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala
 405 410 415
 Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu
 420 425 430
 Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu
 435 440 445
 Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu
 450 455 460
 Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg
 465 470 475 480
 Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly
 485 490 495
 Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu
 500 505 510
 Glu Ala Thr Ser Leu
 515

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "oligonucleotide used to modify hTERT cDNA nucleotides 779 to 781 from GCG to CAT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

CCGGCCACCC CCCATATGCC GCGCGCTCCC

30

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: /note= "oligonucleotide used to create expression vectors pGRN127, pGRN128 and pGRN130"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

TCCGCACGTG GGAAGCCCTG GCAGATCTGA ATTCCACCAT GCCGCGCGCT CCCCCTG

58

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: /note= "oligonucleotide used to create expression vectors pGRN129 and pGRN130"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

CGGGACGGGC TGCTCCTGCG TTTGGTGGAC GCGTTCTTGT TGGTGACACC TCACCTCACC

60

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

Asn Ser Ala Val Asp
1 5

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1154
- (D) OTHER INFORMATION: /note= "fusion protein composed of hTRT protein sequence, vector sequences, the Myc epitope and His6 tag"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

```

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
1          5          10          15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
          20          25          30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
          35          40          45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
          50          55          60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65          70          75          80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
          85          90          95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
          100          105          110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
          115          120          125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
          130          135          140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
          145          150          155          160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
          165          170          175

```

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp Leu Glu Gln Lys
 1125 1130 1135

Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
 1140 1145 1150

His His

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1200
- (D) OTHER INFORMATION: /note= "fusion protein composed of His6 and Anti-Xpress tags, enterokinase cleavage site and full length hTERT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met Pro Arg Gly Ser His His His His His His Gly Met Ala Ser Met
 1 5 10 15

Thr Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Leu
 20 25 30

Asp Pro-Ser Ser Arg Ser Ala Ala Gly Thr Met Glu Phe Ala Ala Ala
 35 40 45

Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro
 50 55 60

Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser
 65 70 75 80

Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val
 85 90 95

Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro
 100 105 110

Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp
 115 120 125

Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys
 130 135 140

Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly
 145 150 155 160

Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg
 165 170 175

Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro
 180 185 190
 Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu
 195 200 205
 Leu Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys
 210 215 220
 Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly
 225 230 235 240
 Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro
 245 250 255
 His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn
 260 265 270
 His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly
 275 280 285
 Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys
 290 295 300
 Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly
 305 310 315 320
 Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg
 325 330 335
 Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser
 340 345 350
 Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly
 355 360 365
 Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro
 370 375 380
 Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu
 385 390 395 400
 Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser
 405 410 415
 Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile
 420 425 430
 Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro
 435 440 445
 Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu
 450 455 460
 Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His
 465 470 475 480
 Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg
 485 490 495

Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp
 500 505 510
 Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln
 515 520 525
 Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly
 530 535 540
 Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys
 545 550 555 560
 Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu
 565 570 575
 Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro
 580 585 590
 Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile
 595 600 605
 Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu
 610 615 620
 Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg
 625 630 635 640
 Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly
 645 650 655
 Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala
 660 665 670
 Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg
 675 680 685
 Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met
 690 695 700
 Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu
 705 710 715 720
 Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu
 725 730 735
 Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp
 740 745 750
 Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln
 755 760 765
 Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala
 770 775 780
 Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile
 785 790 795 800
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln
 805 810 815

Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser
 820 825 830
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu
 835 840 845
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser
 850 855 860
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe
 865 870 875 880
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys
 885 890 895
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu
 900 905 910
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp
 915 920 925
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His
 930 935 940
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro
 945 950 955 960
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro
 965 970 975
 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala
 980 985 990
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu
 995 1000 1005
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala
 1010 1015 1020
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg
 1025 1030 1035 1040
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp
 1045 1050 1055
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile
 1060 1065 1070
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro
 1075 1080 1085
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile
 1090 1095 1100
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala
 1105 1110 1115 1120
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu
 1125 1130 1135

Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg
 1140 1145 1150

His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln
 1155 1160 1165

Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu
 1170 1175 1180

Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1185 1190 1195 1200

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1189
- (D) OTHER INFORMATION: /note= "fusion protein composed of
 melittin signal sequence and full length
 hTRT protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
 1 5 10 15

Ser Tyr Ile Tyr Ala Asp Pro Ser Ser Arg Ser Ala Ala Gly Thr Met
 20 25 30

Glu Phe Ala Ala Ala Ser Thr Gln Arg Cys Val Leu Leu Arg Thr Trp
 35 40 45

Glu Ala Leu Ala Pro Ala Thr Pro Ala Met Pro Arg Ala Pro Arg Cys
 50 55 60

Arg Ala Val Arg Ser Leu Leu Arg Ser His Tyr Arg Glu Val Leu Pro
 65 70 75 80

Leu Ala Thr Phe Val Arg Arg Leu Gly Pro Gln Gly Trp Arg Leu Val
 85 90 95

Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala Leu Val Ala Gln Cys Leu
 100 105 110

Val Cys Val Pro Trp Asp Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe
 115 120 125

Arg Gln Val Ser Cys Leu Lys Glu Leu Val Ala Arg Val Leu Gln Arg
 130 135 140

Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu
 145 150 155 160
 Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val
 165 170 175
 Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu Arg Gly Ser Gly
 180 185 190
 Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp Val Leu Val His
 195 200 205
 Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala Pro Ser Cys Ala
 210 215 220
 Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln
 225 230 235 240
 Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys
 245 250 255
 Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly Val Pro Leu Gly
 260 265 270
 Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser
 275 280 285
 Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu
 290 295 300
 Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg
 305 310 315 320
 Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala
 325 330 335
 Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser
 340 345 350
 His Pro Ser Val Gly Arg Gln His His Ala Gly Pro Pro Ser Thr Ser
 355 360 365
 Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu
 370 375 380
 Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro
 385 390 395 400
 Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg
 405 410 415
 Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr
 420 425 430
 Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro
 435 440 445
 Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val
 450 455 460

Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala
 465 470 475 480
 Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu
 485 490 495
 Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His
 500 505 510
 Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg
 515 520 525
 Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe
 530 535 540
 Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu
 545 550 555 560
 Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp
 565 570 575
 Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala Ala Glu His Arg
 580 585 590
 Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp Leu Met Ser Val
 595 600 605
 Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr
 610 615 620
 Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys
 625 630 635 640
 Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg
 645 650 655
 Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala
 660 665 670
 Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg
 675 680 685
 Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg
 690 695 700
 Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser
 705 710 715 720
 Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser
 725 730 735
 Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu
 740 745 750
 Arg Val Arg Ala Gln Asp Pro Pro Glu Leu Tyr Phe Val Lys Val
 755 760 765
 Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu
 770 775 780

Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg
 785 790 795 800
 Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe
 805 810 815
 Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln
 820 825 830
 Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val
 835 840 845
 Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp
 850 855 860
 Val Phe Leu Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys
 865 870 875 880
 Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr
 885 890 895
 Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala
 900 905 910
 Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu
 915 920 925
 Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu
 930 935 940
 Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr
 945 950 955 960
 Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe
 965 970 975
 Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu
 980 985 990
 Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg
 995 1000 1005
 Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly
 1010 1015 1020
 Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His
 1025 1030 1035 1040
 Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr
 1045 1050 1055
 Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys
 1060 1065 1070
 Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe
 1075 1080 1085
 Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu
 1090 1095 1100

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..92
(D) OTHER INFORMATION: /note= "oligonucleotide used to create
expression vectors pGRN128 and pGRN129"

CTGCCCTCAG ACTTCAAGAC CATCCTGGAC TACAGGACG ACGATGACAA ATGAATTCAG 60
ATGTGCGGGC GCCACCGCGG TGGAGCTCCA GC 92

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..53
(D) OTHER INFORMATION: /note= "mutagenic oligo used to add a CSP45I site at the C-terminus of hTERT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

CTTCAAGACC ATCCTGGACT TTCGAAACGC GGCCGCCACC GCGGTGGAGC TCC

53

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: /note= "oligonucleotide RA45"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

GCCACCCCCG CGCTGCCTCG AGCTCCCCGC TGC

33

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /note= "primer hTR+1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GGGGAAGCTT TAATACGACT CACTATAGGG TTGCGGAGGG TGGGCCTG

48

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "primer hTR+445"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

CCCCGGATCC TGCGCATGTG TGAGCCGAGT CCTGGG

36

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: /note= "synthetic telomerase product"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

ATTCCGTCGA GCAGAGTTAG GGTTAGGGTT AGGGTTAGGG TTAGGGTTAG GGTTAGGGTT

60

AG

62

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "primer M2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

AATCCGTCGA GCAGAGTT

18

(2) INFORMATION FOR SEQ ID NO:621:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "primer H3.03"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

TTAGGGTTAG GGTAGGG

18

(2) INFORMATION FOR SEQ ID NO:622:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

AATCCGTCGA GCAGAGGG

18

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

AATCCGTCGA GCAGATAG

18

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /note= "T701 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GGGAGATCTT AATACGACTC ACTATAGATT CAGGCCATGG TGCTGCGCCG GCTGTCAGGC 60
TCCCACGACG TAGTCCATGT TCAC 84

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "reverse01 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GGGTCTAGAT CCGGAGAGT GTCTGGAGCA AG 32

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: /note= "T702 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GGGAGATCTT AATACGACTC ACTATAGATT CAGGCCATGG TGCTGCGCCG GCTGTCAGGG 60
CGGCCTTCTG GACCACGGCA TACC 84

(2) INFORMATION FOR SEQ ID NO:627:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "reverse02 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GGTCTAGACG ATATCCACAG GGCCTGGCGC

30

(2) INFORMATION FOR SEQ ID NO:628:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1407 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..1407
- (D) OTHER INFORMATION: /note= "fusion protein composed of enhanced green fluorescent protein (EGFP) residues, residues encoded by the 5' untranslated region of hTRT mRNA and hTRT protein sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628: -

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	1	5	10	15
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	20	25	30	
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	35	40	45	
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	50	55	60	
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	65	70	75	80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Arg Thr Gln Ile Ser Ser Ser Ser Phe Glu Phe Ala Ala Ala Ser
 245 250 255
 Thr Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala
 260 265 270
 Thr Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu
 275 280 285
 Leu Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg
 290 295 300
 Arg Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala
 305 310 315 320
 Ala Phe Arg Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp
 325 330 335
 Ala Arg Pro Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu
 340 345 350
 Lys Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala
 355 360 365
 Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly
 370 375 380
 Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn
 385 390 395 400

Thr Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu
 405 410 415
 Arg Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala
 420 425 430
 Leu Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro
 435 440 445
 Pro Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His
 450 455 460
 Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His
 465 470 475 480
 Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala
 485 490 495
 Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg
 500 505 510
 Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln
 515 520 525
 Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly
 530 535 540
 Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu
 545 550 555 560
 Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg
 565 570 575
 Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp
 580 585 590
 Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr
 595 600 605
 Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser
 610 615 620
 Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe
 625 630 635 640
 Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg
 645 650 655
 Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu
 660 665 670
 Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys
 675 680 685
 Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu
 690 695 700
 Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro
 705 710 715 720

Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val
 725 730 735
 Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu
 740 745 750
 Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys
 755 760 765
 Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr
 770 775 780
 Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly
 785 790 795 800
 Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu
 805 810 815
 Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
 820 825 830
 Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
 835 840 845
 Phe Phe Tyr Arg Pro Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
 850 855 860
 Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
 865 870 875 880
 Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
 885 890 895
 Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp
 900 905 910
 Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg
 915 920 925
 Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg
 930 935 940
 Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp
 945 950 955 960
 Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp
 965 970 975
 Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr
 980 985 990
 Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile
 995 1000 1005
 Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys
 1010 1015 1020
 Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr
 1025 1030 1035 1040

Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln
 1045 1050 1055
 Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser
 1060 1065 1070
 Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met
 1075 1080 1085
 Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln
 1090 1095 1100
 Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys
 1105 1110 1115 1120
 Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly
 1125 1130 1135
 Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu
 1140 1145 1150
 Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu
 1155 1160 1165
 Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val
 1170 1175 1180
 Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His
 1185 1190 1195 1200
 Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu
 1205 1210 1215
 Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser
 1220 1225 1230
 Val Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys
 1235 1240 1245
 Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu
 1250 1255 1260
 Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu
 1265 1270 1275 1280
 Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe
 1285 1290 1295
 His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser
 1300 1305 1310
 Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly
 1315 1320 1325
 Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala
 1330 1335 1340
 Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His
 1345 1350 1355 1360

Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr
 1365 1370 1375

Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala
 1380 1385 1390

Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1395 1400 1405

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "TS primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

AATCCGTCGA GCAGAGTT

18

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "ACX primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

GCGCGGCTTA CCCTTACCCT TACCCTAACC

30

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "U2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

ATCGCTTCTC GGCCTTTT

18

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "TSU2 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

AATCCGTCGA GCAGAGTTAA AAGGCCGAGA AGCGAT

36

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

Xaa Arg Xaa Xaa Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = Phe or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid, Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

Xaa Arg Xaa Ile Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:635:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Pro Xaa Leu Tyr Phe Xaa Xaa Xaa Asp Xaa Xaa Xaa Cys Tyr Asp Xaa
 1 5 10 15
 Ile

(2) INFORMATION FOR SEQ ID NO:636:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

Lys Xaa Tyr Xaa Gln Xaa Xaa Gly Ile Pro Gln Gly Ser Xaa Leu Ser
 1 5 10 15

Xaa Xaa Leu

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa = hydrophobic amino acid,
Ala, Leu, Ile, Val, Pro, Phe,
Trp or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

Leu Leu Arg Leu Xaa Asp Asp Xaa Leu Xaa Ile Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing
alternative codon distributions for
E. coli (all genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

ATGCCGCGCG CGCCGCGCTG CCGCGCGGTG CGCAGCCTGC TGCGCAGCCA TTATCGCGAA	60
GTGCTGCCGC TGGCGACCTT TGTGCGCCGC CTGGGCCCGC AGGGCTGGCG CCTGGTGCAG	120
CGCGGCGATC CGGCGGCGTT TCGCGCGCTG GTGGCGCAGT GCCTGGTGTG CGTGCCGTGG	180
GATGCGCGCC CGCCGCCGGC GCGCGCGAGC TTTGCCCAGG TGAGCTGCCT GAAAGAACTG	240
GTGGCGCGCG TGCTGCAGCG CCTGTGCGAA CGCGGCGCGA AAAACGTGCT GGCCTTTGGC	300
TTTGCCTGCG TGGATGGCGC GCGCGGCGGC CCGCCGGAAG CGTTTACCAC CAGCGTGCGC	360
AGCTATCTGC CGAACACCGT GACCGATGCG CTGCGCGGCA GCGGCGCGTG GGGCCTGCTG	420
CTGCGCCGCG TGGGCGATGA TGTGCTGGTG CATCTGCTGG CGCGCTGCGC GCTGTTTGTG	480
CTGGTGGCGC CGAGCTGCGC GTATCAGGTG TGCGGCCCGC CGCTGTATCA GCTGGGCGCG	540
GCGACCCAGG CGCGCCCGCC GCCGCATGCG AGCGGCCCGC GCCGCCGCCT GGGCTGCGAA	600
CGCGCGTGGA ACCATAGCGT GCGCGAAGCG GGCCTGCCGC TGGGCCTGCC GGCGCCGGGC	660
GCGCGCCGCG GCGGCGGCAG CGCGAGCCGC AGCCTGCCGC TGCCGAAACG CCCGCGCCGC	720
GGCGCGGCGC CGGAACCGGA ACGCACCCCG GTGGGCCAGG GCAGCTGGGC GCATCCGGGC	780
CGCACCCGCG GCCCGAGCGA TCGCGGCTTT TGCCTGGTGA GCCCGGCGCG CCCGGCGGAA	840
GAAGCGACCA GCCTGGAAGG CGCGCTGAGC GGCACCCGCC ATAGCCATCC GAGCGTGGGC	900
CGCCAGCATC ATGCGGGCCC GCCGAGCAC AGCCGCCCGC CGCGCCCGTG GGATACCCCG	960
TGCCCGCCCG TGTATGCGGA AACCAAACAT TTTCTGTATA GCAGCGGCGA TAAAGAACAG	1020
CTGCGCCCGA GCTTTCTGCT GAGCAGCCTG CGCCCGAGCC TGACCGGCGC GCGCCGCCTG	1080
GTGGAAACCA TTTTCTGGG CAGCCGCCCG TGGATGCCGG GCACCCCGCG CCGCCTGCCG	1140
CGCCTGCCGC AGCGCTATTG GCAGATGCGC CCGCTGTTTC TGGAACTGCT GGGCAACCAT	1200
GCGCAGTGCC CGTATGGCGT GCTGCTGAAA ACCCATTGCC CGCTGCGCGC GCGGCTGACC	1260
CCGGCGGCGG GCGTGTGCGC GCGCGAAAAA CCGCAGGGCA GCGTGCGGC GCGGAAGAA	1320
GAAGATACCG ATCCGCGCCG CCTGGTGCAG CTGCTGCGCC AGCATAGCAG CCCGTGGCAG	1380
GTGTATGGCT TTGTGCGCGC GTGCCTGCGC CGCCTGGTGC CGCCGGGCCT GTGGGGCAGC	1440
CGCCATAACG AACGCCGCTT TCTGCGCAAC ACCAAAAAAT TTATTAGCCT GGGCAAACAT	1500
GCGAAACTGA GCCTGCAGGA ACTGACCTGG AAAATGAGCG TGCGCGATTG CGCGTGGCTG	1560
CGCCGCAGCC CGGGCGTGGG CTGCGTGCCG GCGGCGGAAC ATCGCCTGCG CGAAGAAATT	1620
CTGGCGAAAT TTCTGCATTG GCTGATGAGC GTGTATGTGG TGGAACTGCT GCGCAGCTTT	1680
TTTTATGTGA CCGAAACCAC CTTTCAGAAA AACCGCCTGT TTTTTATCG CAAAAGCGTG	1740
TGGAGCAAAC TGCAGAGCAT TGGCATTGCG CAGCATCTGA AACGCGTGCA GCTGCGCGAA	1800

CTGAGCGAAG CGGAAGTGCG CCAGCATCGC GAAGCGCGCC CGGCGCTGCT GACCAGCCGC	1860
CTGCGCTTTA TTCCGAAACC GGATGGCCTG CGCCCGATTG TGAACATGGA TTATGTGGTG	1920
GGCGCGCGCA CCTTTCGCCG CGAAAAACGC GCGGAACGCC TGACCAGCCG CGTGAAAGCG	1980
CTGTTTAGCG TGCTGAACTA TGAACGCGCG CGCCGCCCGG GCCTGCTGGG CGCGAGCGTG	2040
CTGGGCCTGG ATGATATTCA TCGCGCGTGG CGCACCTTTG TGCTGCGCGT GCGCGCGCAG	2100
GATCCGCCGC CGGAACTGTA TTTTGTGAAA GTGGATGTGA CCGGCGCGTA TGATACCATT	2160
CCGCAGGATC GCCTGACCGA AGTGATTGCG AGCATTATTA AACCGCAGAA CACCTATTGC	2220
GTGCGCCGCT ATGCGGTGGT GCAGAAAGCG GCGCATGGCC ATGTGCGCAA AGCGTTTAAA	2280
AGCCATGTGA GCACCCTGAC CGATCTGCAG CCGTATATGC GCCAGTTTGT GCGCATCTG	2340
CAGGAAACCA GCCCGCTGCG CGATGCGGTG GTGATTGAAC AGAGCAGCAG CCTGAACGAA	2400
GCGAGCAGCG GCCTGTTTGA TGTGTTTCTG CGCTTTATGT GCCATCATGC GGTGCGCATT	2460
CGCGGCAAAA GCTATGTGCA GTGCCAGGGC ATTCCGCAGG GCAGCATTCT GAGCACCTG	2520
CTGTGCAGCC TGTGCTATGG CGATATGGAA AACAACTGT TTGCGGGCAT TCGCCGCGAT	2580
GGCCTGCTGC TCGCCTGGT GGATGATTTT-CTGCTGGTGA CCCC GCATCT GACCCATGCG	2640
AAAACCTTTC TGCGCACCTT GGTGCGCGGC GTGCCGGAAT ATGGCTGCGT GGTGAACCTG	2700
CGCAAAACCG TGGTGAACCT TCCGGTGGAA GATGAAGCGC TGGGCGGCAC CGCGTTTGTG	2760
CAGATGCCGG CGCATGGCCT GTTTCGCTGG TGCGGCCTGC TGCTGGATAC CCGCACCTG	2820
GAAGTGCAGA GCGATTATAG CAGCTATGCG CGCACCAGCA TTCGCGCGAG CCTGACCTTT	2880
AACCGCGGCT TTAAAGCGGG CCGCAACATG CGCCGCAAAC TGTTTGCGT GCTGCGCCTG	2940
AAATGCCATA GCCTGTTTCT GGATCTGCAG GTGAACAGCC TGCAGACCGT GTGCACCAAC	3000
ATTTATAAAA TTCTGCTGCT GCAGGCGTAT CGCTTTCATG CGTGCGTGCT GCAGCTGCCG	3060
TTTCATCAGC AGGTGTGGAA AAACCCGACC TTTTTTCTGC GCGTGATTAG CGATACCGCG	3120
AGCCTGTGCT ATAGCATTCT GAAAGCGAAA AACGCGGGCA TGAGCCTGGG CGCGAAAGGC	3180
GCGGCGGGCC CGCTGCCGAG CGAAGCGGTG CAGTGGCTGT GCCATCAGGC GTTTCTGCTG	3240
AAACTGACCC GCCATCGCGT GACCTATGTG CCGCTGCTGG GCAGCCTGCG CACCGCGCAG	3300
ACCCAGCTGA GCCGCAAACT GCCGGGCACC ACCCTGACCG CGCTGGAAGC GGCGGCGAAC	3360
CCGGCGCTGC CGAGCGATTT TAAAACCATT CTGGAT	3396

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for enteric bacteria (high expressing genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

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GTTCTGCCGC TGGCTACCTT CGTTCGTCGT CTGGGTCCGC AGGGTTGGCG TCTGGTTCAG      120
CGTGGTGACC CGGCTGCTTT CCGTGCTCTG GTTGCTCAGT GCCTGGTTTG CGTTCCGTGG      180
GACGCTCGTC CGCCGCCGGC TGCTCCGTCC TTCCGTCAGG TTTCCTGCCT GAAAGAACTG      240
GTTGCTCGTG TTCTGCAGCG TCTGTGCGAA CGTGGTGCTA AAAACGTTCT GGCTTTCCGT      300
TTGCTCTGTC TGGACGGTGC TCGTGGTGGT CCGCCGGAAG CTTTCACCAC CTCCGTTCGT      360
TCCTACCTGC CGAACACCGT TACCGACGCT CTGCGTGGTT CCGGTGCTTG GGGTCTGCTG      420
CTGCGTCGTG TTGGTGACGA CGTTCTGGTT CACCTGCTGG CTCGTTGCGC TCTGTTTCGT      480
CTGCTTGCTC CGTCCTGCGC TTACCAGGTT TGCGGTCCGC CGCTGTACCA GCTGGGTGCT      540
GCTACCCAGG CTCGTCCGCC GCCGCACGCT TCCGGTCCGC GTCGTCGTCT GGGTTGCGAA      600
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GCTCGTCGTC GTGGTGGTTC CGCTTCCCGT TCCCTGCCGC TGCCGAAACG TCCGCGTCGT      720
GGTGCTGCTC CGGAACCGGA ACGTACCCCG GTTGGTCAGG GTTCCTGGGC TCACCCGGGT      780
CGTACCCGTG GTCCGTCCGA CCGTGGTTTC TCGGTTGTTT CCCC GGCTCG TCCGGCTGAA      840
GAAGCTACCT CCCTGGAAGG TGCTCTGTCC GGTACCCGTC ACTCCCACCC GTCCGTTCGT      900
CGTCAGCACC ACGCTGGTCC GCCGTCCACC TCCCGTCCGC CGCGTCCGTG GGACACCCCG      960
TGCCCCCGCG TTTACGCTGA AACCAAACAC TTCCTGTACT CCTCCGGTGA CAAAGAACAG     1020
CTGCGTCCGT CCTTCCTGCT GTCTCCCTG CGTCCGTCCC TGACCGGTGC TCGTCGTCTG     1080
GTTGAAACCA TCTTCCTGGG TTCCCGTCCG TGGATGCCGG GTACCCCGCG TCGTCTGCCG     1140
CGTCTGCCGC AGCGTACTG GCAGATGCGT CCGCTGTTCC TGGAAGTGT GGGTAACCAC     1200

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GCTCAGTGCC CGTACGGTGT TCTGCTGAAA ACCCACTGCC CGCTGCGTGC TGCTGTTACC	1260
CCGGCTGCTG GTGTTTGCGC TCGTGAAAAA CCGCAGGGTT CCGTTGCTGC TCCGGAAGAA	1320
GAAGACACCG ACCCGCGTCG TCTGGTTCAG CTGCTGCGTC AGCACTCCTC CCCGTGGCAG	1380
GTTTACGGTT TCGTTCGTGC TTGCCTGCGT CGTCTGGTTC CGCCGGGTCT GTGGGGTTCC	1440
CGTCACAACG AACGTCGTTT CCTGCGTAAC ACCAAAAAAT TCATCTCCCT GGGTAAACAC	1500
GCTAAACTGT CCCTGCAGGA ACTGACCTGG AAAATGTCCG TTCGTGACTG CGCTTGCTG	1560
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TTCTACGTTA CCGAAACCAC CTTCCAGAAA AACCGTCTGT TCTTCTACCG TAAATCCGTT	1740
TGGTCCAAAC TGCAGTCCAT CGGTATCCGT CAGCACCTGA AACGTGTTCA GCTGCGTGAA	1800
CTGTCCGAAG CTGAAGTTCG TCAGCACCGT GAAGCTCGTC CGGCTCTGCT GACCTCCCGT	1860
CTGCGTTTCA TCCCGAAACC GGACGGTCTG CGTCCGATCG TTAACATGGA CTACGTTGTT	1920
GGTGCTCGTA CCTTCCGTCG TGAAAAACGT GCTGAACGTC TGACCTCCCG TGTTAAAGCT	1980
CTGTTCTCCG TTCTGAACTA CGAACGTGCT CGTCGTCCGG GTCTGCTGGG TGCTTCCGTT	2040
CTGGGTCTGG ACGACATCCA CCGTGCTTGG CGTACCTTCG TTCTGCGTGT TCGTGCTCAG	2100
GACCCGCCGC CGGAACTGTA CTTGTTAAA GTTGACGTTA CCGGTGCTTA CGACACCATC	2160
CCGCAGGACC GTCTGACCGA AGTTATCGCT TCCATCATCA AACCGCAGAA CACCTACTGC	2220
GTTCGTCGTT ACGCTGTTGT TCAGAAAGCT GCTCACGGTC ACGTTCGTAA AGCTTTCAA	2280
TCCCACGTTT CCACCCTGAC CGACCTGCAG CCGTACATGC GTCAGTTCGT TGCTCACCTG	2340
CAGGAAACCT CCCCCTGCG TGACGCTGTT GTTATCGAAC AGTCCTCCTC CCTGAACGAA	2400
GCTTCCTCCG GTCTGTTTCA CGTTTTCTG CGTTTCATGT GCCACCACGC TGTTTCGTATC	2460
CGTGGTAAAT CCTACGTTCA GTGCCAGGGT ATCCCGCAGG GTTCCATCCT GTCCACCCTG	2520
CTGTGCTCCC TGTGCTACGG TGACATGGAA AACAACTGT TCGCTGGTAT CCGTCGTGAC	2580
GGTCTGCTGC TCGCTCTGGT TGACGACTTC CTGCTGGTTA CCCCACCT GACCCACGCT	2640
AAAACCTTCC TGCGTACCCT GGTTCGTGGT GTTCCGGAAT ACGGTTGCGT TGTTAACCTG	2700
CGTAAAACCG TTGTAACTT CCCGTTGAA GACGAAGCTC TGGGTGGTAC CGCTTTCGTT	2760
CAGATGCCGG CTCACGGTCT GTTCCCGTGG TCGGGTCTGC TGCTGGACAC CCGTACCCTG	2820
GAAGTTCAGT CCGACTACTC CTCCTACGCT CGTACCTCCA TCCGTGCTTC CCTGACCTTC	2880
AACCGTGGTT TCAAAGCTGG TCGTAACATG CGTCGTAAAC TGTTTCGGTGT TCTGCGTCTG	2940
AAATGCCACT CCCTGTTCTT GGACCTGCAG GTTAACTCCC TGCAGACCGT TTGCACCAAC	3000
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TTCCACCAGC AGGTTTGGAA AAACCCGACC TTCTTCCTGC GTGTTATCTC CGACACCGCT      3120
TCCCTGTGCT ACTCCATCCT GAAAGCTAAA AACGCTGGTA TGTCCCTGGG TGCTAAAGGT      3180
GCTGCTGGTC CGCTGCCGTC CGAAGCTGTT CAGTGGCTGT GCCACCAGGC TTTCTGCTG      3240
AAACTGACCC GTCACCGTGT TACCTACGTT CCGCTGCTGG GTTCCCTGCG TACCGCTCAG      3300
ACCCAGCTGT CCCGTAAACT GCCGGGTACC ACCCTGACCG CTCTGGAAGC TGCTGCTAAC      3360
CCGGCTCTGC CGTCCGACTT CAAAACCATC CTGGAC                                3396

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(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for yeast (all genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

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ATGCCAAGAG CTCCAAGATG TAGAGCTGTT AGATCTTTGT TGAGATCTCA TTATAGAGAA      60
GTTTTGCCAT TGGCTACTTT TGTTAGAAGA TTGGGTCCAC AAGGTTGGAG ATTGGTTCAA      120
AGAGGTGATC CAGCTGCTTT TAGAGCTTTG GTTGCTCAAT GTTTGGTTTG TGTTCATGG      180
GATGCTAGAC CACCACCAGC TGCTCCATCT TTAGACAAG TTTCTTGTTT GAAAGAATTG      240
GTTGCTAGAG TTTTGCAAAG ATTGTGTGAA AGAGGTGCTA AAAATGTTTT GGCTTTTGGT      300
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TCTTATTTGC CAAATACTGT TACTGATGCT TTGAGAGGTT CTGGTGCTTG GGGTTTGTG      420
TTGAGAAGAG TTGGTGATGA TGTTTTGGTT CATTTGTTGG CTAGATGTGC TTTGTTTGT      480
TTGGTTGCTC CATCTTGTC TTATCAAGTT TGTGGTCCAC CATTGTATCA ATTGGGTGCT      540
GCTACTCAAG CTAGACCACC ACCACATGCT TCTGSTCCAA GAAGAAGATT GGGTTGTGAA      600
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AGAACTAGAG GTCCATCTGA TAGAGGTTTT TGTGTTGTTT CTCCAGCTAG ACCAGCTGAA      840

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GAAGCTACTT CTTTGGGAAGG TGCTTTGTCT GGTACTAGAC ATTCTCATCC ATCTGTTGGT	900
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TGTCCACCAG TTTATGCTGA AACTAAACAT TTTTGTATT CTTCTGGTGA TAAAGAACAA	1020
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AGATTGCCAC AAAGATATTG GCAAATGAGA CCATTGTTTT TGGAATTGTT GGGTAATCAT	1200
GCTCAATGTC CATATGGTGT TTTGTTGAAA ACTCATTGTC CATTGAGAGC TGCTGTTACT	1260
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GAAGATACTG ATCCAAGAAG ATTGGTTCAA TTGTTGAGAC AACATTCTTC TCCATGGCAA	1380
GTTTATGGTT TTGTTAGAGC TTGTTTGAGA AGATTGGTTC CACCAGGTTT GTGGGGTTCT	1440
AGACATAATG AAAGAAGATT TTTGAGAAAT ACTAAAAAAT TTATTTCTTT GGGTAAACAT	1500
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TTGTCTGAAG CTGAAGTTAG ACAACATAGA GAAGCTAGAC CAGCTTTGTT GACTTCTAGA	1860
TTGAGATTTA TTCCAAAACC AGATGGTTTG AGACCAATTG TTAATATGGA TTATGTTGTT	1920
GGTGCTAGAA CTTTTAGAAG AGAAAAAGA GCTGAAAGAT TGACTTCTAG AGTTAAAGCT	1980
TTGTTTTCTG TTTTGAATTA TGAAAGAGCT AGAAGACCAG GTTTGTTGGG TGCTTCTGTT	2040
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GATCCACCAC CAGAATTGTA TTTTGTTAAA GTTGATGTTA CTGGTGCTTA TGATACTATT	2160
CCACAAGATA GATTGACTGA AGTTATTGCT TCTATTATTA AACCACAAAA TACTTATTGT	2220
GTTAGAAGAT ATGCTGTTGT TCAAAAAGCT GCTCATGGTC ATGTTAGAAA AGCTTTTAAA	2280
TCTCATGTTT CTACTTTGAC TGATTTGCAA CCATATATGA GACAATTTGT TGCTCATTTG	2340
CAAGAAACTT CTCCATTGAG AGATGCTGTT GTTATTGAAC AATCTTCTTC TTTGAATGAA	2400
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AGAGGTAAAT CTTATGTTCA ATGTCAAGGT ATTCCACAAG GTTCTATTTT GTCTACTTTG	2520
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AGAAAACTG TTGTTAATTT TCCAGTTGAA GATGAAGCTT TGGGTGGTAC TGCTTTTGT	2760
CAAATGCCAG CTCATGGTTT GTTCCATGG TGTGGTTTGT TGTTGGATAC TAGAACTTTG	2820
GAAGTTCAAT CTGATTATTC TTCTTATGCT AGAACTTCTA TTAGAGCTTC TTTGACTTTT	2880
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GCTGCTGGTC CATTGCCATC TGAAGCTGTT CAATGGTTGT GTCATCAAGC TTTTTTGTG	3240
AAATTGACTA GACATAGAGT TACTTATGTT CCATTGTTGG GTTCTTTGAG AACTGCTCAA	3300
ACTCAATTGT CTAGAAAATT GCCAGGTACT ACTTTGACTG CTTTGAAGC TGCTGCTAAT	3360
CCAGCTTTGC CATCTGATTT TAAAACTATT TTGGAT	3396

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "hTRT-encoding sequence employing alternative codon distributions for yeast (high expressing genes)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

ATGCCAAGAG CTCCAAGATG TAGAGCTGTT AGATCTTTGT TGAGATCTCA CTACAGAGAA	60
GTTTTGCCAT TGGCTACTTT CGTTAGAAGA TTGGGTCCAC AAGGTTGGAG ATTGGTTCAA	120
AGAGGTGACC CAGCTGCTTT CAGAGCTTTG GTTGCTCAAT GTTTGGTTTG TGTTCATGG	180
GACGCTAGAC CACCACCAGC TGCTCCATCT TTCAGACAAG TTTCTTGTTT GAAGGAATTG	240
GTTGCTAGAG TTTTGCAAAG ATTGTGTGAA AGAGGTGCTA AGAACGTTTT GGCTTTCCGT	300
TTGCTTTTGT TGGACGGTGC TAGAGGTGGT CCACCAGAAG CTTTCACTAC TTCTGTTAGA	360
TCTTACTTGC CAAACACTGT TACTGACGCT TTGAGAGGTT CTGGTGCTTG GGGTTTGTG	420
TTGAGAAGAG TTGGTGACGA CGTTTTGGTT CACTTGTTGG CTAGATGTGC TTTGTTCCGT	480

TTGGTTGCTC CATCTTGTGC TTACCAAGTT TGTGGTCCAC CATTGTACCA ATTGGGTGCT	540
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AGAGCTTGGA ACCACTCTGT TAGAGAAGCT GGTGTTCCAT TGGGTTTGCC AGCTCCAGGT	660
GCTAGAAGAA GAGGTGGTTC TGCTTCTAGA TCTTTGCCAT TGCCAAAGAG ACCAAGAAGA	720
GGTGCTGCTC CAGAACCAGA AAGAACTCCA GTTGGTCAAG GTTCTTGGGC TCACCCAGGT	780
AGAACTAGAG GTCCATCTGA CAGAGGTTTC TGTGTTGTTT CTCCAGCTAG ACCAGCTGAA	840
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AGACAACACC ACGCTGGTCC ACCATCTACT TCTAGACCAC CAAGACCATG GGACACTCCA	960
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GTTGAAACTA TTTTCTTGGG TTCTAGACCA TGGATGCCAG GTACTCCAAG AAGATTGCCA	1140
AGATTGCCAC AAAGATACTG GCAAATGAGA CCATTGTTCT TGGAATTGTT GGGTAACCAC	1200
GCTCAATGTC CATACGGTGT TTTGTTGAAG ACTCACTGTC CATTGAGAGC TGCTGTTACT	1260
CCAGCTGCTG GTGTTTGTGC TAGAGAAAAG CCACAAGGTT CTGTTGCTGC TCCAGAAGAA	1320
GAAGACACTG ACCCAAGAAG ATTGGTTCAA TTGTTGAGAC AACACTCTTC TCCATGGCAA	1380
GTTTACGGTT TCGTTAGAGC TTGTTTGAGA AGATTGGTTC CACCAGGTTT GTGGGGTTCT	1440
AGACACAACG AAAGAAGATT CTTGAGAAAC ACTAAGAAGT TCATTTCTTT GGGTAAGCAC	1500
GCTAAGTTGT CTTTGCAAGA ATTGACTTGG AAGATGTCTG TTAGAGACTG TGCTTGGTTG	1560
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TTGTCTGAAG CTGAAGTTAG ACAACACAGA GAAGCTAGAC CAGCTTTGTT GACTTCTAGA	1860
TTGAGATTCA TTCCAAAGCC AGACGGTTTG AGACCAATTG TTAACATGGA CTACGTTGTT	1920
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TTGGGTTTGG ACGACATTCA CAGAGCTTGG AGAACTTTCTG TTTTGAGAGT TAGAGCTCAA	2100
GACCCACCAC CAGAATTGTA CTTGTTAAG GTTGACGTTA CTGGTGCTTA CGACACTATT	2160
CCACAAGACA GATTGACTGA AGTTATTGCT TCTATTATTA AGCCACAAA CACTTACTGT	2220
GTTAGAAGAT ACGCTGTTGT TCAAAAGGCT GCTCACGGTC ACGTTAGAAA GGCTTTCAAG	2280
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CAAGAAACTT CTCCATTGAG AGACGCTGTT GTTATTGAAC AATCTTCTTC TTTGAACGAA	2400
GCTTCTTCTG GTTTGTTCGA CGTTTTCTTG AGATTCATGT GTCACCACGC TGTTAGAATT	2460
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CAAATGCCAG CTCACGTTT GTTCCCATGG TGTGGTTTGT TGTGGACAC TAGAACTTTG	2820
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GCTGCTGGTC CATTGCCATC TGAAGCTGTT CAATGGTTGT GTCACCAAGC TTTCTTGTTG	3240
AAGTTGACTA GACACAGAGT TACTTACGTT CCATTGTTGG GTTCTTTGAG AACTGCTCAA	3300
ACTCAATTGT CTAGAAAGTT GCCAGGTACT ACTTTGACTG CTTTGGGAAGC TGCTGCTAAC	3360
CCAGCTTTGC CATCTGACTT CAAGACTATT TTGGAC	3396

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3396
- (D) OTHER INFORMATION: /note= "generic" hTRT protein encoding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

ATGCCACGTG CCCACGTTG TCGTGCCGTT CGTCTTTGT TGC GTTCTCA CTACCGTGAA	60
GTTTTGCCAT TGGCCACCTT CGTTCGTCGT TTGGGTCCAC AAGGTTGGCG TTTGGTTCAA	120
CGTGGTGATC CAGCCGCCTT CCGTGCCTTG GTTGCCCAAT GTTTGGTTTG TGTTCCATGG	180

GATGCCCGTC CACCACCAGC CGCCCCATCT TTCCGTCAAG TTTCTTGTTT GAAAGAATTG	240
GTTGCCCGTG TTTTGCAACG TTTGTGTGAA CGTGGTGCCA AAAACGTTTT GGCCTTCGGT	300
TTCGCCTTGT TGGATGGTGC CCGTGGTGGT CCACCAGAAG CCTTCACCAC CTCTGTTCTG	360
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CGTGCCTGGA ACCACTCTGT TCGTGAAGCC GGTGTTCCAT TGGGTTTGCC AGCCCCAGGT	660
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GGTGCCGCCC CAGAACCAGA ACGTACCCCA GTTGGTCAAG GTTCTTGGGC CCACCCAGGT	780
CGTACCCGTG GTCCATCTGA TCGTGGTTTC TGTGTTGTTT CTCCAGCCCG TCCAGCCGAA	840
GAAGCCACCT CTTTGGAAGG TGCCTTGTCT GGTACCCGTC ACTCTACCC ATCTGTTGGT	900
CGTCAACACC ACGCCGGTCC ACCATCTACC TCTCGTCCAC CACGTCCATG GGATACCCCA	960
TGTCCACCAG TTTACGCCGA AACCAAACAC TTCTTGTTACT CTTCTGGTGA TAAAGAACAA	1020
TTGCGTCCAT CTTTCTTGTT GTCTTCTTTG CGTCCATCTT TGACCGGTGC CCGTCGTTTG	1080
GTTGAAACCA TTTTCTTGGG TTCTCGTCCA TGGATGCCAG GTACCCACG TCGTTTGCCA	1140
CGTTTGCCAC AACGTTACTG GCAAATGCGT CCATTGTTCT TGAATTGTT GGGTAACCAC	1200
GCCCAATGTC CATACGGTGT TTTGTTGAAA ACCCACTGTC CATTGCGTGC CGCCGTTACC	1260
CCAGCCGCCG GTGTTTGTGC CCGTGAAAAA CCACAAGGTT CTGTTGCCG CCGAGAAGAA	1320
GAAGATACCG ATCCACGTCG TTTGGTTCAA TTGTTGCGTC AACACTCTTC TCCATGGCAA	1380
GTTTACGGTT TCGTTCGTGC CTGTTGCGT CGTTTGGTTC CACCAGGTTT GTGGGGTTCT	1440
CGTCACAACG AACGTCGTTT CTGCGTAAC ACCAAAAAT TCATTTCTTT GGGTAAACAC	1500
GCCAAATTGT CTTTGCAAGA ATTGACCTGG AAAATGTCTG TTCGTGATTG TGCCTGGTTG	1560
CGTCGTTCTC CAGGTGTTGG TTGTGTTCCA GCCGCCGAAC ACCGTTTGCG TGAAGAAATT	1620
TTGGCCAAAT TCTTGCACTG GTTGATGTCT GTTTACGTTG TTGAATTGTT GCGTTCTTTC	1680
TTCTACGTTA CCGAAACCAC CTTCCAAAAA AACC GTTTGT TCTTCTACCG TAAATCTGTT	1740
TGGTCTAAAT TGCAATCTAT TGGTATTCGT CAACACTTGA AACGTGTTCA ATTGCGTGAA	1800
TTGTCTGAAG CCGAAGTTCG TCAACACCGT GAAGCCCGTC CAGCCTTGTT GACCTCTCGT	1860
TTGCGTTTCA TTCCAAAACC AGATGGTTTG CGTCCAATTG TTAACATGGA TTACGTTGTT	1920
GGTGCCCGTA CCTTCCGTCG TGAAAAACGT GCCGAACGTT TGACCTCTCG TGTTAAAGCC	1980
TTGTTCTCTG TTTTGAAC TAACACGTGCC CGTCGTCCAG GTTTGTTGGG TGCCTCTGTT	2040

TTGGGTTTGG ATGATATTCA CCGTGCCTGG CGTACCTTCG TTTTGCCTGT TCGTGCCCAA	2100
GATCCACCAC CAGAATTGTA CTTCGTAAAA GTTGATGTTA CCGGTGCCTA CGATACCATT	2160
CCACAAGATC GTTTGACCGA AGTTATTGCC TCTATTATTA AACCACAAA CACCTACTGT	2220
GTTCGTCTGT ACGCCGTTGT TCAAAAAGCC GCCCACGGTC ACGTTCGTAA AGCCTTCAAA	2280
TCTCAGTTTT CTACCTTGAC CGATTTGCAA CCATACATGC GTCAATTCGT TGCCCACTTG	2340
CAAGAAACCT CTCCATTGCG TGATGCCGTT GTTATTGAAC AATCTTCTTC TTTGAACGAA	2400
GCCTCTTCTG GTTTGTTTGA TGTTCCTTG CGTTTCATGT GTCACCACGC CGTTCGTATT	2460
CGTGGTAAAT CTTACGTTCA ATGTCAAGGT ATTCCACAAG GTTCTATTTT GTCTACCTTG	2520
TTGTGTTCTT TGTGTTACGG TGATATGGAA AACAAATTGT TCGCCGGTAT TCGTCGTGAT	2580
GGTTTGTGTT TGCCTTTGGT TGATGATTTT TTGTTGGTTA CCCCACACTT GACCCACGCC	2640
AAAACCTTCT TGCCTACCTT GGTTCGTGGT GTTCCAGAAT ACGGTTGTGT TGTAACTTG	2700
CGTAAAACCG TTGTAACTT CCCAGTTGAA GATGAAGCCT TGGGTGGTAC CGCCTTCGTT	2760
CAAATGCCAG CCCACGGTTT GTTCCCATGG TGTGGTTTGT TGTGGATAC CCGTACCTTG	2820
GAAGTTCAAT CTGATTACTC TTCTTACGCC CGTACCTCTA TTCGTGCCTC TTTGACCTTC	2880
AACCGTGGTT TCAAAGCCGG TCGTAACATG CGTCGTAAAT TGTCGGTGT TTTGCGTTTG	2940
AAATGTCACT CTTTGTCTT GGATTTGCAA GTTAACTCTT TGCAAACCGT TTGTACCAAC	3000
ATTACAAAA TTTTGTGTGTT GCAAGCCTAC CGTTTCCACG CCTGTGTTTT GCAATTGCCA	3060
TTCCACCAAC AAGTTTGGAA AAACCCAACC TTCTTCTTGC GTGTTATTTT TGATACCGCC	3120
TCTTTGTGTT ACTCTATTTT GAAAGCCAAA AACGCCGGTA TGCTTTGGG TGCCAAAGGT	3180
GCCGCCGGTC CATTGCCATC TGAAGCCGTT CAATGGTTGT GTCACCAAGC CTTCTTGTG	3240
AAATTGACCC GTCACCGTGT TACCTACGTT CCATTGTTGG GTTCTTTGCG TACCGCCCAA	3300
ACCCAATTGT CTCGTAAATT GCCAGGTACC ACCTTGACCG CCTTGAAGC CGCCGCCAAC	3360
CCAGCCTTGC CATCTGATTT CAAAACCATT TTGGAT	3396

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: /note= "oligonucleotide 1B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

CCAGCGGCAG AACTTCGCGA TAGTGGGAAC GCAGCAGGGA ACGAACAGCA CGGCAACGCG 60
GAGCACGCGG CATATGGTCG ACTCTAGAGC TCCCGCGTGC 100

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 1T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GCACGCGGGA GCTCTAGAGT CGACCATATG CCGCGTGCTC CGCGTTGCCG TGCTGTTCGT 60
TCCCTGCTGC GTTCCCACTA TCGCGAAGTT 90

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 2B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

GGCACTGAGC AACCAGAGCA CGGAAAGCAG CCGGGTCACC ACGCTGAACC AGACGCCAAC 60
CCTGCGGGCC CAGACGACGA ACGAAGGTAG 90

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 2T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

```
CTGCCGCTGG CTACCTTCGT TCGTCGTCTG GGCCCGCAGG GTTGGCGTCT GGTTCAGCGT      60
GGTGACCCGG CTGCTTTCCG TGCTCTGGTT                                         90
```

(2) INFORMATION FOR SEQ ID NO:647:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 3B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

```
GAACACGAGC AACCAGTTCT TTCAGGCAGG AACCTGACG GAAGGACGGA GCAGCCGGCG      60
GCGGACGAGC GTCGCACGGA ACGCAAACCA                                         90
```

(2) INFORMATION FOR SEQ ID NO:648:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 3T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GCTCAGTGCC TGGTTTGCCT TCCGTGGGAC GCTCGTCCGC CGCCGGGTGC TCCGTCCTTC 60
 CGTCAGGTTT CCTGCCTGAA AGAACTGGTT 90

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 4B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

ATGCTTCCGG CGGACCACCA CGAGCACCGT CCAGCAGAGC GAAACCGAAA GCCAGAACGT 60
 TTTTAGCACC ACGTTCGCAC AGACGCTGCA 90

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 4T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GCTCGTGTTC TGCAGCGTCT GTGCGAACGT GGTGCTAAAA ACGTTCTGGC TTTCGGTTTC 60
 GCTCTGCTGG ACGGTGCTCG TGGTGGTCCG 90

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 5B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

CAACACGACG CAGCAGCAGA CCCCAAGCAC CGGAACCACG CAGAGCGTCG GTAACGGTGT	60
TCGGCAGGTA GGAACGAACG GAGGTGGTGA	90

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 5T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

CCGGAAGCAT TCACCACCTC CGTTCGTTCC TACCTGCCGA ACACCGTTAC CGACGCTCTG	60
CGTGGTTCCG GTGCTTGGGG TCTGCTGCTG	90

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 6B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

GCGGCGGACC ACAAACCTGG TAAGCGCAGG ACGGAGCAAC CAGAACGAAC AGAGCGCAAC 60
GAGCCAGCAG GTGAACCAGA ACGTCGTCAC 90

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 6T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

CGTCGTGTTG GTGACGACGT TCTGGTTCAC CTGCTGGCTC GTTGCGCTCT GTTCGTTCTG 60
GTTGCTCCGT CCTGCGCTTA CCAGTTTGT 90

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 7B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GGTTCCAAGC ACGTTCGCAA CCCAGACGAC GACGCGGACC GGAAGCGTGC GGCGGCGGAC 60
GAGCCTGGGT AGCAGCACCC AGCTGGTACA 90

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 7T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

```
GGTCCGCCGC TGTACCAGCT GGGTGCTGCT ACCCAGGCTC GTCCGCCGCC GCACGCTTCC      60
GGTCCGCGTC GTCGTCTGGG TTGCGAACGT                                         90
```

(2) INFORMATION FOR SEQ ID NO:657:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 8B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

```
GCAGCGGCAG GGAACGGGAA GCGGAACCAC CACGACGACG AGCACCCGGA GCCGGCAGAC      60
CCAGCGGAAC ACCAGCTTCA CGAACGGAGT                                         90
```

(2) INFORMATION FOR SEQ ID NO:658:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 8T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

GCTTGAACC ACTCCGTTTCG TGAAGCTGGT GTTCCGCTGG GTCTGCCGGC TCCGGGTGCT 60
 CGTCGTCGTG GTGGTTCCGC TTCCCGTTCC 90

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 9B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GACCACGGGT ACGACCCGGG TGAGCCCAGG AACCTGACC AACCGGGGTA CGTTCCGGTT 60
 CCGGAGCAGC ACCACGACGC GGACGTTTCG 90

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 9T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

CTGCCGCTGC CGAAACGTCC GCGTCGTGGT GCTGCTCCGG AACCGGAACG TACCCCGGTT 60
 GGTCAGGGTT CCTGGGCTCA CCCGGGTCGT 90

(2) INFORMATION FOR SEQ ID NO:661:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 10B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

AGTGACGGGT GCCGGACAGA GCACCTTCCA GGGAGGTAGC TTCTCAGCC GGACGAGCCG 60
GGGAAACAAC GCAGAAACCA CGGTCCGACG 90

(2) INFORMATION FOR SEQ ID NO:662:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 10T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

ACCCGTGGTC CGTCCGACCG TGGTTTCTGC GTTGTTTCCC CGGCTCGTCC GGCTGAAGAA 60
GCTACCTCCC TGAAGGTGC TCTGTCCGGC 90

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 11B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

```
AAACCGGCGG GCACGGGGTG TCCCACGGAC GCGGCGGACG GGAGGTGGAC GGCGGACCAG      60
CGTGGTGCTG ACGACCAACG GACGGGTGGG                                     90
```

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 11T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

```
ACCGTCACT CCCACCGTC CGTTGGTCGT CAGCACCACG CTGGTCCGCC GTCCACCTCC      60
CCTCCGCCGC GTCCGTGGGA CACCCCGTGC                                     90
```

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 12B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

```
TCAGGGACGG ACGCAGGGAG GACAGCAGGA AGGACGGACG CAGCTGTTCT TTGTCACCGG      60
AGGAGTACAG GAAGTGTTTG GTTTCAGCGT                                     90
```

(2) INFORMATION FOR SEQ ID NO:666:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 12T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

CCGCCGGTTT ACGCTGAAAC CAAACACTTC CTGTACTCCT CCGGTGACAA AGAACAGCTG 60
CGTCCGTCCT TCCTGCTGTC CTCCTGCGT 90

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 13B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GCTGCGGCAG ACGCGGCAGA CGACGCGGGG TGCCCGGCAT CCACGGACGG GAACCCAGGA 60
AGATAGTTTC AACCAGACGA CGAGCACCGG 90

(2) INFORMATION FOR SEQ ID NO:668:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 13T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

CCGTCCCTGA CCGGTGCTCG TCGTCTGGTT GAAACTATCT TCCTGGGTTC CCGTCCGTGG 60
 ATGCCGGGCA CCCC GCGTCG TCTGCCGCGT 90

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 14B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GCGGGCAGTG GGTTCCTCAGC AGAACACCAT ACGGGCACTG AGCGTGTTG CCCAGCAGTT 60
 CCAGGAACAG CGGACGCATC TGCCAGTAAC 90

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 14T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

CTGCCGCAGC GTTACTGGCA GATGCGTCCG CTGTTCTCTGG AACTGCTGGG CAACCACGCT 60
 CAGTGCCCGT ATGGTGTCTCT GCTGAAAACC 90

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 15B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

GGTCGGTATC TTCTTCTTCC GGAGCAGCAA CGGAACCCTG CGGTTTTTCA CGAGCGCAAA 60
CACCAGCAGC CGGGGTAACA GCAGCAGCA 90

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 15T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

CACTGCCCGC TCGTGCTGC TGTTACCCCG GCTGCTGGTG TTTGCGCTCG TGAAAAACCG 60
CAGGGTTCCG TTGCTGCTCC GGAAGAAGAA 90

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 16B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GCGGAACCAG ACGACGCAGG CATGCACGAA CGAAACCGTA AACCTGCCAC GGGGAGGAGT 60
 GCTGACGCAG CAGCTGAACC AGACGACGCG 90

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 16T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GATACCGACC CGCGTCGTCT GGTTTCAGCTG CTGCGTCAGC ACTCCTCCCC GTGGCAGGTT 60
 TACGGTTTCG TTCGTGCATG CCTGCGTCGT 90

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 17B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GGGACAGTTT AGCGTGTTTA CCCAGGGAGA TGAATTTTTT GGTGTTACGC AGGAAACGAC 60
 GTTCGTTGTG ACGGGAACCC CACAGACCCG 90

(2) INFORMATION FOR SEQ ID NO:676:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 17T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

CTGGTTCCGC CGGGTCTGTG GGGTTCCCGT CACAACGAAC GTCGTTTCCT GCGTAACACC 60
AAAAAATTCA TCTCCCTGGG TAAACACGCT 90

(2) INFORMATION FOR SEQ ID NO:677:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 18B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

GGTGTTCAGC AGCCGGAACG CAACCAACAC CCGGAGAACG ACGCAGCCAA GCGCAGTCAC 60
GAACGGACAT TTTCCAGGTC AGTTCCTGCA 90

(2) INFORMATION FOR SEQ ID NO:678:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 18T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

AAACTGTCCC TGCAGGAACT GACCTGGAAA ATGTCCGTTT GTGACTGCGC TTGGCTGCGT 60
CGTTCTCCGG GTGTTGGTTG CGTTCCGGCT 90

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 19B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

CGGTAACGTA GAAGAAGGAA CGCAGCAGTT CAACAACGTA TACGGACATC AGCCAGTGCA 60
GGPATTTAGC CAGGATTCTT TCACGCAGAC 90

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 19T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GCTGAACACC GTCTGCGTGA AGAAATCCTG GCTAAATTCC TGCAGTGGCT GATGTCCGTA 60
TACGTTGTTG AACTGCTGCG TTCCTTCTTC 90

(2) INFORMATION FOR SEQ ID NO:681:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 20B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GTTTCAGGTG CTGACGGATA CCGATGGACT GCAGTTTGGA CCAAACGGAT TTACGGTAGA 60
AGAACAGACG GTTTTTCTGG AAGGTGGTTT 90

(2) INFORMATION FOR SEQ ID NO:682:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: /note= "oligonucleotide 20T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

TACGTTACCG AAACCACCTT CCAGAAAAC CGTCTGTTCT TCTACCGTAA ATCCGTTTGG 60
TCCAAACTGC AGTCCATCGG TATCCGTCAG 90

(2) INFORMATION FOR SEQ ID NO:683:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: /note= "oligonucleotide 21B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

GATGAAACGC AGACGGGAGG TCAGCAGAGC CGGACGAGCT TCACGGTGCT GACGAACTTC 60
 AGCTTCGGAC AGTTCACGCA GCTGAACAC 89

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 21T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

CACCTGAAAC GTGTCAGCT GCGTGAAGCTG TCCGAAGCTG AAGTTCGTCA GCACCGTGAA 60
 GCTCGTCCGG CTCTGCTGAC CTCCCGTCTG 90

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 22B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

TCAGACGCTC AGCAGTTTT TCACGACGGA AGGTACGAGC ACCAACAACG TAGTCCATGT 60
 TTACGATCGG ACGCAGACCG TCCGGTTTCG 90

(2) INFORMATION FOR SEQ ID NO:686:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 22T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

```
CGTTTCATCC CGAAACCGGA CGGTCTGCGT CCGATCGTAA ACATGGACTA CGTTGTTGGT    60
GCTCGTACCT TCCGTCGTGA AAAACGTGCT                                     90
```

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 23B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

```
CGTCCAGACC CAGAACGGAA GCACCCAGCA GACCCGGACG ACGAGCACGT TCGTAGTTCA    60
GAACGGAGAA CAGAGCTTTA ACACGGGAGG                                     90
```

(2) INFORMATION FOR SEQ ID NO:688:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 23T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GAGCGTCTGA CCTCCCGTGT TAAAGCTCTG TTCTCCGTTC TGAACCTACGA ACGTGCTCGT 60
 CGTCCGGGTC TGCTGGGTGC TTCCGTTCTG 90

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 24B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

CGGTAACGTC AACTTTAACG AAGTACAGTT CCGGCGGCGG GTCCTGAGCA CGAACACGCA 60
 GAACGAAGGT ACGCCAAGCA CGGTGGATGT 90

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 24T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GGTCTGGACG ACATCCACCG TGCTTGGCGT ACCTTCGTTC TCGTGTTTCG TGCTCAGGAC 60
 CCGCCGCCGG AACTGTACTT CGTTAAAGTT 90

(2) INFORMATION FOR SEQ ID NO:691:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..90
(D) OTHER INFORMATION: /note= "oligonucleotide 25B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

CGTAACGACG AACGCAGTAG GTGTTCTGCG GTTTGATGAT GGAAGCGATA ACTTCGGTCA 60
GACGGTCCTG CGGGATGGTG TCGTACGCGC 90

(2) INFORMATION FOR SEQ ID NO:692:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..90
(D) OTHER INFORMATION: /note= "oligonucleotide 25T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

GACGTTACCG GCGCGTACGA CACCATCCCG CAGGACCGTC TGACCGAAGT TATCGCTTCC 60
ATCATCAAAC CGCAGAACAC CTACTGCGTT 90

(2) INFORMATION FOR SEQ ID NO:693:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 26B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

GACGCATGTA CGGCTGCAGG TCGGTCAGGG TGGAAACGTG GGATTGAAT GCTTTACGAA 60
CGTGACCGTG AGCAGCTTTC TGAACAACAG 90

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 26T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

CGTCGTTACG CTGTTGTTCA GAAAGCTGCT CACGGTCAGG TTCGTAAAGC ATTCAAATCC 60
CAGGTTTCCA CCCTGACCGA CCTGCAGCCG 90

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 27B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GACCGGAGGA AGCTTCGTTC AGGGAGGAGG ACTGTTTCGAT AACAACAGCG TCACGCAGCG 60
GGGAGGTTTC CTGCAGGTGA GCAACGAACT 90

(2) INFORMATION FOR SEQ ID NO:696:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..90
(D) OTHER INFORMATION: /note= "oligonucleotide 27T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

TACATGCGTC AGTTCGTTGC TCACCTGCAG GAAACCTCCC CGCTGCGTGA CGCTGTTGTT 60
ATCGAACAGT CCTCCTCCCT GAACGAAGCT 90

(2) INFORMATION FOR SEQ ID NO:697:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..90
(D) OTHER INFORMATION: /note= "oligonucleotide 28B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

AACCCTGCGG GATACCCTGG CACTGAACGT AGGATTTACC ACGGATACGA ACAGCGTGGT 60
GGCACATGAA ACGCAGGAAA ACGTCGAACA 90

(2) INFORMATION FOR SEQ ID NO:698:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 28T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

```
TCCTCCGGTC TGTTGACGT TTCCTGCGT TTCATGTGCC ACCACGCTGT TCGTATCCGT      60
GGTAAATCCT ACGTTCAGTG CCAGGGTATC                                     90
```

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 29B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

```
CCAGCAGCAG ACCGTCACGA CGGATACCAG CGAACAGTTT GTTTTCCATG TCACCGTAGC      60
ACAGGGAGCA CAGCAGGGTG GACAGGATGG                                     90
```

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 29T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

```
CCGCAGGGTT CCATCCTGTC CACCCTGCTG TGCTCCCTGT GCTACGGTGA CATGGAAAAC      60
AAACTGTTCG CTGGTATCCG TCGTGACGGT                                     90
```

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 30B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

```
CGTATTCGG AACACCACGA ACCAGGGTAC GCAGGAAGGT TTAGCGTGG GTCAGGTGCG      60
GAGTAACCAG CAGGAAGTCG TCAACCAGAC                                     90
```

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 30T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

```
CTGCTGCTGC GTCTGGTTGA CGACTTCCTG CTGGTTACTC CGCACCTGAC CCACGCTAAA      60
ACCTTCCTGC GTACCCTGGT TCGTGGTGTGTT                                     90
```

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 31B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GAGCCGGCAT CTGAACGAAA GCGGTGCCAC CCAGAGCTTC GTCTTCAACC GGAAGTTAA 60
 CAACGGTTTT ACGCAGGTTT ACAACGCAAC 90

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 31T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

CCGGAATACG GTTGC GTTGT AAACCTGCGT AAAACCGTTG TTAAGTTCCC GGTGAAGAC 60
 GAAGCTCTGG GTGGCACCGC TTTCGTTTCA 90

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 32B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GGATGGAGGT ACGAGCGTAG GAGGAGTAGT CGGACTGAAC TTCCAGGGTA CGGGTGTCCA 60
 GCAGCAGACC GCACCACGGG AACAGACCGT 90

(2) INFORMATION FOR SEQ ID NO:706:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 32T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

```
ATGCCGGCTC ACGGTCTGTT CCCGTGGTGC GGTCTGCTGC TGGACACCCG TACCCTGGAA      60
GTTCA GTCCG ACTACTCCTC CTACGCTCGT                                     90
```

(2) INFORMATION FOR SEQ ID NO:707:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 33B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

```
GGGAGTGGCA TTTCAGACGC AGAACACCGA ACAGTTTACG ACGCATGTTA CGACCAGCTT      60
TGAAACCACG GTTGAAGGTC AGGGAAGCAC                                     90
```

(2) INFORMATION FOR SEQ ID NO:708:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 33T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

ACCTCCATCC GTGCTTCCCT GACCTTCAAC CGTGGTTTCA AAGCTGGTCG TAACATGCGT 60
CGTAAACTGT TCGGTGTTCT GCGTCTGAAA 90

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 34B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

ACGCGTGGAA ACGGTAAGCC TGCAGCAGCA GGATTTTGTA GATGTTGGTG CAAACGGTCT 60
GCAGGGAGTT TACCTGCAGG TCCAGGAACA 90

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 34T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

TGCCACTCCC TGTTCTGGA CCTGCAGGTA AACTCCCTGC AGACCGTTTG CACCAACATC 60
TACAAAATCC TGCTGCTGCA GGCTTACCGT 90

(2) INFORMATION FOR SEQ ID NO:711:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..90
(D) OTHER INFORMATION: /note= "oligonucleotide 35B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

```
AGTAGCACAG GGAAGCGGTG TCGGAGATAA CACGCAGGAA GAAGGTCGGG TTTTCCAAA      60
CCTGCTGGTG GAACGGCAGC TGCAGAACGC                                     90
```

(2) INFORMATION FOR SEQ ID NO:712:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..90
(D) OTHER INFORMATION: /note= "oligonucleotide 35T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

```
TTCCACGCGT GCGTTCTGCA GCTGCCGTTT CACCAGCAGG TTTGGAAAAA CCCGACCTTC      60
TTCCTGCGTG TTATCTCCGA CACCGCTTCC                                     90
```

(2) INFORMATION FOR SEQ ID NO:713:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 36B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

```
GGCACAGCCA CTGAACAGCT TCGGACGGCA GCGGACCAGC AGCACCTTTA GCACCCAGGG      60
ACATACCAGC GTTTTTAGCT TTCAGGATGG      90
```

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: /note= "oligonucleotide 36T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

```
CTGTGCTACT CCATCCTGAA AGCTAAAAAC GCTGGTATGT CCCTGGGTGC TAAAGGTGCT      60
GCTGGTCCGC TGCCGTCCGA AGCTGTTTCA      90
```

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: /note= "oligonucleotide 37B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

```
ACAGCTGGGT CTGAGCGGTA CGCAGGGAC CCAGCAGCGG AACGTAGGTA ACACGGTGAC      60
GGGTCAGTTT CAGCAGGAAA GCCTGGT      87
```

(2) INFORMATION FOR SEQ ID NO:716:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..87
 (D) OTHER INFORMATION: /note= "oligonucleotide 37T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

```
TGGCTGTGCC ACCAGGCTTT CCTGCTGAAA CTGACCCGTC ACCGTGTTAC CTACGTTCCG      60
CTGCTGGGTT CCCTGCGTAC CGCTCAG                                           87
```

(2) INFORMATION FOR SEQ ID NO:717:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..63
 (D) OTHER INFORMATION: /note= "oligonucleotide 38B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

```
ACGGCAGAGC CGGGTTAGCA GCAGCTTCCA GAGCGGTCAG GGTGGTACCC GGCAGTTTAC      60
GGG                                                                    63
```

(2) INFORMATION FOR SEQ ID NO:718:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: /note= "oligonucleotide 38T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

ACCCAGCTGT CCCGTAAACT GCCGGGTACC ACCCTGACCG CTCTGGAAGC TGCTGCTAAC 60
CCGG 64

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /note= "oligonucleotide 39B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GCGTGCCTCG AGGAATTCGG ATCCATTAGT CCAGGATGGT TTTGAAGTCG 50

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: /note= "oligonucleotide 39T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

CTCTGCCGTC CGACTTCAAA ACCATCCTGG ACTAATGGAT CCGAATTCCT CGAGGCACGC 60

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..3451
- (D) OTHER INFORMATION: /note= "hTRT sequence employing codon distribution preferentially used by highly expressed genes in E. coli containing SacI and XhoI sites"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

GCACGCGGGA GCTCTAGAGT CGACCATATG CCGCGTGCTC CCGGTTGCCG TGCTGTTCTG	60
TCCCTGCTGC GTTCCCACTA TCGCGAAGTT CTGCCGCTGG CTACCTTCGT TCGTCGCTCG	120
GGCCCGCAGG GTTGGCGTCT GGTTCAGCGT GGTGACCCGG CTGCTTTCCG TGCTCTGGTT	180
GCTCAGTGCC TGGTTTGCGT TCCGTGGGAC GTCGTCCGC CGCCGGCTGC TCCGTCTTC	240
CGTCAGGTTT CCTGCCTGAA AGAACTGGTT GTCGTGTTT TGCAGCGTCT GTGCGAACGT	300
GGTGCTAAAA ACGTTCTGGC TTTCGGTTTC GCTCTGCTGG ACGGTGCTCG TGGTGGTCCG	360
CCGGAAGCAT TCACCACCTC CGTTCGTTCC TACCTGCCGA ACACCGTTAC CGACGCTCTG	420
CGTGGTTCCG CTGCTTGGGG TCTGCTGCTG CGTCGTGTTG GTGACGACGT TCTGGTTCAC	480
CTGCTGGCTC GTTGGCGTCT GTTCGTTCTG GTTGCTTCGT CCTGCGCTTA CCAGGTTTGT	540
GGTCCGCCGC TGTACCAGCT GGGTGCTGCT ACCCAGGCTC GTCCGCCGCC GCACGCTTCC	600
GGTCCGCGTC GTCGTCTGGG TTGCGAACGT GCTTGAACC ACTCCGTTCC TGAAGCTGGT	660
GTTCGGCTGG GTCTGCCGGC TCCGGGTGCT CGTCGTCTGT GTGGTTCCGC TTCCCGTTCC	720
CTGCCGCTGC CGAAACGTCC GCGTCGTGGT GCTGCTCCGG AACCGGAACG TACCCCGGTT	780
GGTCAGGGTT CCTGGGCTCA CCGGGGTGCT ACCCGTGGTC CGTCCGACCG TGGTTTCTGC	840
GTTGTTTCCC CGGCTCGTCC GGCTGAAGAA GCTACCTCCC TGGAAGGTGC TCTGTCCGGC	900
ACCCGTCACT CCCACCCGTC CGTTGGTCGT CAGCAACAG CTGGTCCGCC GTCCACCTCC	960
CGTCCGCCGC GTCCGTGGGA CACCCCGTGC CCGCCGTTT ACGCTGAAAC CAAACACTTC	1020
CTGTACTCCT CCGGTGACAA AGAACAGCTG CGTCCGTCTT TCCTGCTGTC CTCCTGCGT	1080
CCGTCCCTGA CCGGTGCTCG TCGTCTGGTT GAAACTATCT TCCTGGGTTT CCGTCCGTGG	1140
ATGCCGGGCA CCGCGCTCG TCTGCCGCGT CTGCCGCAGC GTTACTGGCA GATGCGTCCG	1200

CTGTTCTG	AACTGCTGGG	CAACCACGCT	CAGTGCCCGT	ATGGTGTTCT	GCTGAAAACC	1260
CACTGCCCCG	TGCGTGCTGC	TGTTACCCCG	GCTGCTGGTG	TTTGCCTCG	TGAAAAACCG	1320
CAGGGTTCCG	TTGCTGCTCC	GGAAGAAGAA	GATACCGACC	CGCGTCGTCT	GGTTCAGCTG	1380
CTGCGTCAGC	ACTCCTCCCC	GTGGCAGGTT	TACGGTTTCG	TTCTGTCATG	CCTGCGTCGT	1440
CTGGTTCCCG	CGGGTCTGTG	GGGTTCCCGT	CACAACGAAC	GTCGTTTCCT	GCGTAACACC	1500
AAAAAATTCA	TCTCCCTGGG	TAAACACGCT	AAACTGTCCC	TGCAGGAACT	GACCTGGAAA	1560
ATGTCCGTTT	GTGACTGCGC	TTGGCTGCGT	CGTTCTCCGG	GTGTTGGTTG	CGTTCCGGCT	1620
GCTGAACACC	GTCTGCGTGA	AGAAATCCTG	GCTAAATTCC	TGCACTGGCT	GATGTCCGTA	1680
TACGTTGTTG	AACTGCTGCG	TTCCTTCTTC	TACGTTACCG	AAACCACCTT	CCAGAAAAAC	1740
CGTCTGTTCT	TCTACCGTAA	ATCCGTTTGG	TCCAAACTGC	AGTCCATCGG	TATCCGTCAG	1800
CACCTGAAAC	GTGTTTCACT	GCGTGAAGTG	TCCGAAGCTG	AAGTTCGTCA	GCACCGTGAA	1860
GCTCGTCCGG	CTCTGCTGAC	CTCCCGTCTG	CGTTTCATCC	CGAAACCGGA	CGGTCTGCGT	1920
CCGATCGTAA	ACATGGACTA	CGTTGTTGGT	GCTCGTACCT	TCCGTCGTGA	AAAACGTGCT	1980
GAGCGTCTGA	CCTCCCGTGT	TAAAGCTCTG	TTCTCCGTTT	TGAACTACGA	ACGTGCTCGT	2040
CGTCCGGGTC	TGCTGGGTGC	TTCCGTTCTG	GGTCTGGACG	ACATCCACCG	TGCTTGGCGT	2100
ACCTTCGTTT	TGCGTGTTCT	TGCTCAGGAC	CCGCCGCCGG	AACTGTACTT	CGTTAAAGTT	2160
GACGTTACCG	GCGCGTACGA	CACCATCCCG	CAGGACCGTC	TGACCGAAGT	TATCGCTTCC	2220
ATCATCAAAC	CGCAGAACAC	CTACTGCGTT	CGTCGTTACG	CTGTTGTTCA	GAAAGCTGCT	2280
CACGGTCACG	TTGTAAGGC	ATTCAAATCC	CACGTTTCCA	CCCTGACCGA	CCTGCAGCCG	2340
TACATGCGTC	AGTTGCTTGC	TCACCTGCAG	GAAACCTCCC	CGCTGCGTGA	CGCTGTTGTT	2400
ATCGAACAGT	CCTCCTCCCT	GAACGAAGCT	TCCTCCGGTC	TGTTGACAGT	TTTCTGCGT	2460
TTCATGTGCC	ACCACGCTGT	TCGTATCCGT	GGTAAATCCT	ACGTTCACTG	CCAGGGTATC	2520
CCGCAGGGTT	CCATCCTGTC	CACCCTGCTG	TGCTCCCTGT	GCTACGGTGA	CATGGAAAAC	2580
AAACTGTTCT	CTGGTATCCG	TCGTGACGGT	CTGCTGCTGC	GTCTGGTTGA	CGACTTCCTG	2640
CTGGTTACTC	CGCACCTGAC	CCACGCTAAA	ACCTTCCTGC	GTACCCTGGT	TCGTGGTGTT	2700
CCGGAATACG	GTTGCGTTGT	AAACCTGCGT	AAAACCGTTG	TTAACTTCCC	GGTTGAAGAC	2760
GAAGCTCTGG	GTGGCACCCG	TTTCGTTTCA	ATGCCGGCTC	ACGGTCTGTT	CCCGTGGTGC	2820
GGTCTGCTGC	TGGACACCCG	TACCCTGGAA	GTTTCACTCCG	ACTACTCCTC	CTACGCTCGT	2880
ACCTCCATCC	GTGCTTCCCT	GACCTTCAAC	CGTGGTTTCA	AAGCTGGTCT	TAACATGCGT	2940
CGTAAACTGT	TCGGTGTTCT	GCGTCTGAAA	TGCCACTCCC	TGTTCTGGA	CCTGCAGGTA	3000
AACTCCCTGC	AGACCGTTTG	CACCAACATC	TACAAAATCC	TGCTGCTGCA	GGCTTACCGT	3060

```

TTCCACGCGT GCGTTCTGCA GCTGCCGTTT CACCAGCAGG TTTGGAAAAA CCCGACCTTC 3120
TTCCTGCGTG TTATCTCCGA CACCGCTTCC CTGTGCTACT CCATCCTGAA AGCTAAAAAC 3180
GCTGGTATGT CCCTGGGTGC TAAAGGTGCT GCTGGTCCGC TGCCGTCCGA AGCTGTTTAC 3240
TGGCTGTGCC ACCAGGCTTT CCTGCTGAAA CTGACCCGTC ACCGTGTTAC CTACGTTCCG 3300
CTGCTGGGTT CCCTGCGTAC CGCTCAGACC CAGCTGTCCC GTAAACTGCC GGTACCACC 3360
CTGACCGCTC TGGAAGCTGC TGCTAACCCG GCTCTGCCGT CCGACTTCAA AACCATCCTG 3420
GACTAATGGA TCCGAATTCC TCGAGGCACG C 3451

```

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "antisense oligonucleotide
corresponding to positions
31-60 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

GGCATCGCGG GGGTGGCCGG GGCCAGGGCT

30

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "antisense oligonucleotide
corresponding to positions
496-525 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GCGCAGCGTG CCAGCAGGTG AACCAGCAGC

30

(2) INFORMATION FOR SEQ ID NO:724:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "antisense oligonucleotide
corresponding to positions
631-660 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

GCCCGTTCGC ATCCCAGACG CCTTCGGGGT

30

(2) INFORMATION FOR SEQ ID NO:725:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "antisense oligonucleotide
corresponding to positions
646-675 of hTRT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

ACGCTATGGT TCCAGGCCCCG TTCGCATCCC

30

(2) INFORMATION FOR SEQ ID NO:726:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: /note= "sequence present in pGRN176 but not pGRN175"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

```

GTGGCGGAGG GACTGGGGAC CCGGGCACCG GTCCTGCCCC TTCACCTTCC AGTCCGCCT      60
CGTCCGCGCG GAACCCCGCC CCGTCCCGAA CCCTTCCCGG GTCCCCGGCC CAGCCCCTTC    120
CGGG                                              124

```

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 1-300 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 630
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at position 630 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 649..663
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 649-663 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 674..688
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 674-688 may be present or absent"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 701..706
- (D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 701-706 may be present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 771..790

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 771-790 may be
present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 887..937

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 887-937 may be
present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 965..994

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 965-994 may be
present or absent"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1018..1027

(D) OTHER INFORMATION: /product= "OTHER"
/note= "Xaa at positions 1018-1027 may
be present or absent"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5						10					15

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20						25					30	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			35					40					45		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			50					55					60		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65						70					75				80

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			85							90				95	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100						105					110	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			115						120					125	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			130					135					140		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
145						150					155				160

[illegible]

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	485	490	495
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	500	505	510
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	515	520	525
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	530	535	540
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	545	550	555
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	565	570	575
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	580	585	590
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	595	600	605
Xaa Xaa Xaa Xaa Xaa Phe Phe Tyr Xaa Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa	610	615	620
Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	625	630	635
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	645	650	655
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	660	665	670
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	675	680	685
Xaa Xaa Xaa Arg Xaa Xaa Pro Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	690	695	700
Xaa Xaa Arg Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	705	710	715
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	725	730	735
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	740	745	750
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	755	760	765
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	770	775	780
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	785	790	795
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	800		

Xaa	Xaa	Xaa	Tyr	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				805						810					815
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			820					825						830	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			835					840					845		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			850					855					860		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			865					870					875		880
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				885						890					895
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				900						905					910
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				915						920					925
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Gly	Xaa
				930					935				940		
Xaa	Gln	Gly	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
	945					950						955			960
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				965						970					975
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				980						985					990
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Asp	Xaa	Leu	Xaa	Xaa	Xaa
				995					1000				1005		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				1010					1015				1020		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys
				1025									1035		1040